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121 DIYAMKVWKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
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                                                                                                                                                                               241 GSAAKANSNKAYNAKLPIGTPDYMAPEVLTVMNGDGKGTYRLDCDWWSVGVIAYEMIYGR 300
                                                                                                                                                                                                                                                              301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
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                                                                            DLLSLLMRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240
                                                                                                                                                        241 GSAAKWNSNKWVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
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DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
                                                                                                   181 DLLSLINRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
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PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
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PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
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Anderson, David W.
Zhong, Mei
Catterton, Elina
Ji, Weizhen
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Spytek, Kimberly A.
Edinger, Shlomit R.
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Leach, Martin D.
Agee, Michele L.
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Malyankar, Uriel M.
Ort, Tatiana
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Li, Li
121
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PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
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Pred. No. 4.9e-189;
1; Mismatches 1; Indels 0
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OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CD1
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CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                        TRIBOULEY, Catherine M. CHAWLA, Narinder K. YAO, Monique G. LU, Dyung Aina M. GREENWALD, Sara R. RAMKUMAR, Jayalaxmi GRIFFIN, Jennifer A.
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APPLICANT: BLLIOTY, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
                                                     Sequence 7, Application US/10311034 Publication No. US20040023242A1 GENERAL INFORMATION:
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RECIPON, Shirley A.
AZIMZAI, Yalda
POLICKY, Jennifer L.
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                                                                                                             APPLICANT: INCYTE GENOMICS, INC
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
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TANG, Y. Tom
BARDON.
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LAL, Preeti
BANDMAN, Olga
BOROWSKY, Mark L.
AU-YOUNG, Janice
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Best Local Similarity 99.6
Matches 495; Conservative
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SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 497
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ORGANISM: Homo sapiens
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APPLICANT: Yu, Xuanchuan
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APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVEXTON: No. US20020123622Alel Human Kinases and Polynucleotides Encoding t
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US 60/258,335
PRIOR APPLICATION NUMBER: US 60/258,335
PRIOR APPLICATION NUMBER: US 60/258,335
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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Pred. No. 6.3e-177;
2; Mismatches 0;
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99.6%; Pred. No. 6.7e-177;
iive 2; Mismatches 0;
          PRIOR FILLING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.6%;
Matches 466; Conservative
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                                                                                                                                   TYPE: PRT
ORGANISM: homo sapiens
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ORGANISM: homo sapiens
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Best Local Similarity
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Publication No. US20020123622A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yu, Kuanchuan
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. US20020123622A1e1 Human Kinases and Polymucleotides Encoding
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/28,946
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 124
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PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-10-09
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-09
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Matches 466; Conservative
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ORGANISM: Homo sapiens
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US-10-262-511-4
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CD1
US-10-415-011-21
             PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/245,708
PRIOR APPLICATION NUMBER: US 60/247,672
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/249,565
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL PROGRAM
LENGTH: 2054
   APPLICATION NUMBER: US 60/244,068
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.6%;
Matches 466; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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                                                                   ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
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                                                                                                                DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
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DLLSLLMRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                                                  ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
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FILE REFERENCE: PI-0262 USN
CURRENT APPLICATION NUMBER: US/10/415,011
CURRENT FILING DATE: 2003-04-18
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FILING DATE: 2001-10-20
APPLICATION NUMBER: US 60/242,410
FILING DATE: 2000-10-20
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BANDWAN, Olga
TRIBOULEX, Catherine M.
LAL, Preeti G.
RECIPON, Shirley A.
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; Publication No. US20040053394A1
; GENERAL INFORMATION:
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APPLICANT: GURURAJAN, Rajagopal
APPLICANT: BAUGHN, Mariah R.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: XU, Yuning
APPLICANT: YO, Woning
APPLICANT: YAVIZU, Chandra S.
APPLICANT: YAO, Wonique G.
APPLICANT: YAO, Monique G.
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THORNTON, Michael B.
SWARNAKER Anita
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KHAN, Farrah A.
ISON, Craig H.
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NGUYEN, Danniel B.
GANDHI, Ameena R.
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BOROWSKY, Mark L.
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US20020160483A1el Human Myotonic Dystrophy Type Prot
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Length 2054;
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                                                            Indels
   Score 2440; DB 15;
Pred. No. 6.7e-177;
2; Mismatches 0;
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; Publication No. US20020160483A1
; Publication No. US20020160483A1
; APPLICANT: KAPELER-LIBERMANN, Rosana
; TITLE OF INVENTION: 11245, A No. US20020160483A1,
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERBNCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; CURRENT APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2001-10-23
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121 DIYAMKVWKKKALLAQEQVSFFEBERNILSRSTSPWIPQLQYAFQDKNHLYLMEBYQPGG 180
                                                                                      61 ECSQPALMKIKHVSNFVRKYSDTIABLQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
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                                  1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
                                                                   ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
                                                                                                                                      DIYAMKVMKKKALLLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG
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Publication No. US20040197825A1
GENERAL INFORMATION:
APPLICANT: Karicheti, Venkateswarlu
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Eliasof, Scott D.
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US-10-325-490-12
i Sequence 12, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
i APPLICANT: Milennium Pharmaceuticals, Inc
i APPLICANT: Milennium Pharmaceuticals, Inc
i APPLICANT: Rosenfeld, Julie Beth
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
TITLE OF INVENTION: 32838,336 and 52908
; FILE REFERENCE: MPIO1-294PIRNM
CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2001-12-19
; PRIOR PELING DATE: 2001-12-19
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                                                                                                                                  93.4%; Score 2430; DB 13;
99.1%; Pred. No. 3.9e-176;
iive 3; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 2053
                  2.1
                                                                                                                                                                   Matches 464; Conservative
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver.
SEQ ID NO 2
                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo Sapiens
US-10-325-430-12
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                                                 LENGTH: 2053
                                                                                       ; ORGANISM: Ho
US-10-017-216-2
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Pred. No. 3.9e-176;
3; Mismatches 1;
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Pred. No. 2.9e-175;
3; Mismatches 1;
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APPLICANT: WHYTE, DAVID
APPLICANT: WANNING, GERARD
APPLICANT: CAENBREEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REPERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT APPLICATION NUMBER: 60/395,632
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SOFTWARE: Patentin version 3.2
LENGTH: 2055
PRIOR FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.1%;
Matches 464; Conservative
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Best Local Similarity 98.9
Matches 464; Conservative
                                              ; SEQ ID NO 52
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-52
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Best Local Similarity
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US-10-618-941-67
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1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE 60

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APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Stone, David
APPLICANT: Grose, William M
APPLICANT: Grose, William M
APPLICANT: Black Milliam M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spytek, Kimberly A
APPLICANT: Spytek, Kimberly A
APPLICANT: Spytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Sylek, Kinderly A
APPLICANT: Sylek, Sinderly A
APPLICANT: Sylek, Silakets, Sichard A
TITLE OF INVENTION: NO. US20040043926Alel Proteins and Nucleic Acids Encoding Same
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181 GDLLSLINRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVD
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                                                                                                          61 ECSQPALMKIKHVSNPVRK-YSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKAT
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CURRENT FILING DATE: 2001-09-26
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PRIOR PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR FILLING DATE: 2000-09-27
PRIOR FILLING DATE: 2000-09-27
PRIOR FILLING DATE: 2000-09-27
PRIOR FILLING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR PILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR PILLING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-28
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PRIOR PILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: 60/326,483

PRIOR PILING DATE: 2001-10-02

PRIOR PILING DATE: 2000-10-02

PRIOR PILING DATE: 2002-04-10-09

PRIOR PILING DATE: 2002-05-10-09

PRIOR PILING DATE: 2002-05-10-09

PRIOR PILING DATE: 2002-05-10-09

PRIOR PILING DATE: 2002-05-10-09

PRIOR PILING DATE: 2002-05-16

PRIOR PILING DATE: 2002-04-17

PRIOR PLING DATE: 2002-04-17

PRIOR PLING DATE: 2002-04-19

PRIOR PLING DATE: 2002-04-19

PRIOR PILING DATE: 2002-04-19

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PRIOR PILING DATE: 2002-04-19

PRIOR PILING DATE: 2001-00-09

PRIOR PILING DATE: 2001-00-05

PRIOR PILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Age, Michele L.
APPLICANT: Age, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
THE REPERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
                                                                                                                                                                                                                                                                     Miller, Charles E. Rastelli, Luca Stone, David J. Pena, Carol E. A. Shenoy, Suresh G.
    Malyankar, Uriel M
                                                                                                                    Zerhusen, Bryan D.
Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets, Richard
                                                                                                                                                                                                  Zhong, Mei
Catterton, Elina
                                                                                  Gorman, Linda
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US-10-262-511-2
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                        PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,399
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR PRIOR FILING DATE: 2001-10-06
PRIOR PRIOR DATE: 2001-10-06
PRIOR PRIOR DATE: 2001-03-16
PRIOR FILING DATE: 2001-05-31
PRIOR PILING DATE: 2001-05-31
PRIOR PILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARR: PRECRILIN VET: 2.1
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Publication No. US2004003823A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICATION NUMBER: 60/238,321
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ORGANISM: Homo sapiens
US-09-964-956-11
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  DB 15; Length 2053;
Query Match 92.7%; Score 2412.5; DB 15; Lengt Best Local Similarity 98.9%; Pred. No. 8.4e-175; Matches 463; Conservative 3; Mismatches 1; Indels
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Guo, Xiaojia (Sasha) Patturajan, Meera Spytek, Kimberly A. Edinger, Shlomit R. Ellerman, Karen

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241 GSAAKMISNKAVNAKLPIGTPDYMAPEVLTVANGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
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                                                                   Score 2412.5; DB 11; Length 2066;
Pred. No. 8.5e-175;
3; Mismatches 1; Indels 1; (
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Job time : 148 secs
                                                                        Query Match 92.7%;
Best Local Similarity 98.9%;
Matches 463; Conservative
; ORGANISM: Homo sapiens
US-09-964-956-9
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241 GSAAKMISIK-VNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 299
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843.195 Million cell updates/sec
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Sequence 2, Ap
Sequence 1, Ap
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Sequence 6, A
Sequence 8511
Sequence 4, A
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Sequence 6
Sequence 2
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2602
1 MLKFKYGARNPLDAGAAEPI......CSRILPSVYAKGSARGRCWL
                                                                                                                                                                           March 18, 2005, 15:31:31; Search time 44 Seconds
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/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/Barrus_COMB.pep:*
/cgm2_6/ptodata/1/iaa/Pcrus_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-238-709-2

US-10-028-946-4

US-10-028-946-4

US-10-028-946-4

US-10-28-10-4

US-09-916-204-4

US-10-282-048-2

US-09-916-204-4

US-09-916-204-6

US-08-685-871-2

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US-08-685-871-5

US-08-6
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Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
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No.
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28 770.5 29.7 638 2 00.6 4 US-08-981-7984-11 Sequence 21, A 20 771.5 29.7 638 2 00.0 60.6 22-6994-11 Sequence 11, A 20 771.5 29.7 638 2 00.0 60.2 29.9 11.0 20.0 20.0 20.0 20.0 20.0 20.0 20.0	Sequence 21, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 13, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 18, Appli Sequence 17, Appli	NUCLEIC KINASE PROTEINS, AND USES	DB 4; Length 497;
28 790.5 29 771.5 31 760.5 32 771.5 33 77.15 33 77.11.5 34 771.1 38 683 39 683 39 683 39 683 39 683 39 683 39 683 39 683 39 683 39 683 39 683 39 683 39 683 30 771.5 38 771.1	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ALIGNMENTS 1804471A 1t al 1 HUMAN KINASE PROTEINS, 1 LECULES ENCODING HUMAN 10S/09/804,471A 13-13 18 Version 4.0	100.0%; Score 2602; DB 4; Length 100.0%; Pred. No. 1.5e-242; ative 0; Mismatches 0; Indels PLDAGAAEPIANRASRIALFPGGKPPFWTOQOMSPLSR
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                                                                                                                                                                            Sequence 2, Application US/10238709

Patent No. 668018

GENERAL INFORMATION:

APPLICANT: WEBSITER, Marion et al

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THERED BY

TITLE OF INVENTION: THERED IV

CURRENT APPLICATION NUMBER: US/10/238,709

CURRENT APPLICATION NUMBER: US/10/238,709

CURRENT FILING DATE: 2002-09-11

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
                                            ECSQPALMKIKHVSNFVRKYSDTIAELQPSAKDFEVRSLVGCGHPAEVQVVREKAIG 120
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Best Local Similarity 100.
Matches 497; Conservative
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; ORGANISM: Human
US-10-238-709-2
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APPLICANT: Wiranda, Maricar
TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT PAPLICATION NUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LIENGTH: 1958
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Patent No. 6734009

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wiranda, Maricar
APPLICANT: Wiranda, Maricar
APPLICANT: Friddle, Carl Johan
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. 673400991 Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
PROFILE REFERENCE: AD 10 NOS: 4
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Best Local Similarity 99.6%; Pred. No. 5.3e-226;
Matches 466; Conservative 2; Mismatches 0;
Sequence 4, Application US/10028946
Patent No. 6734009
GENERAL INFORMATION:
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND INTILE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND INTILE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND INTILE OF INVENTION NUMBER: US/10/238,709

CURRENT FILING DATE: 2002-09-11

NUMBER OF SEQ ID NOS: 4

SOFTWARR: FastSEQ for Windows Version 4.0

SEQ ID NO 4
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                                                                DIYAMKVMKKKALLAQEQVSFFBEERNILSRSTSPWIPQLQYAFQDKNHLYLVMBYQPGG
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87.3%; Score 2271.5; DB 4;
Best Local Similarity 87.3%; Pred. No. 1.2e-210;
Matches 432; Conservative 27; Mismatches 35;
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480 ILQSIYAEGSAGGHC 494
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Sequence 4, Application US/09804471A

Patent No. 6479269

GENERAL INFORMATION:

APPLICANT: WEBSTER, Marion et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOO1164

CURRENT APPLICATION NUMBER: US/09/804,471A

CURRENT APPLICATION NUMBER: 2001-03-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FRSESEQ for Windows Version 4.0
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                                                                                                                                                  93.8%; Score 2440; DB 4; Length 2054; 99.6%; Pred. No. 5.7e-226; ive 2; Mismatches 0; Indels 0
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SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 2
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Matches 432; Conservative
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                                                              TYPE: PRT
CRGANISM: homo sapiens
US-10-028-946-2
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Best Local Simil
Matches 466; C
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US-09-804-471A-4
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US-09-804-471A-4
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TYPE: PRT
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Sequence 2, Application US/09916204

Sequence 2, Application US/09916204

Sequence 2, Application US/09916204

Sequence 2, Application US/09916204

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

THEREFERICE:

TITLE OF INVENTION:

THEREFERICE:

CURRENT APPLICATION NUMBER: US/09/916,204

CURRENT FILING DATE:

SOUTHORS OF SEQ ID NOS: 6

NUMBER OF SEQ ID NOS: 6

SOUTHORS EASTSEQ FOR WINDOWS VERSION 4.0
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SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360
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Best Local Similarity 99.6
Matches 251, Conservative
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ORGANISM: Human
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Sequence 2, Application US/10282048
Patent No. 6692948
GENERAL INFORMATION:
PAPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

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Sequence 4, Application US/09916204
| Sequence 4, Application US/09916204
| Patent No. 6638745
| GENERAL INFORMATION:
| APPLICANT: WEI, Ming-Hui et al.
| TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: CLOOLIGACIP
| CURRENT APPLICATION NUMBER: US/09/916,204
| CURRENT APPLICATION NUMBER: US/09/916,204
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
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                                                                                                                                                                                                                                                                                                                               Score 1284; DB 4;
Pred. No. 1.1e-115;
1; Mismatches 0;
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Best Local Similarity 90.4%; Pred. No. 1.2e-105;
Matches 227; Conservative 13; Mismatches 11;
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOLIGEOTO-DIV
CURRENT APPLICATION NUMBER: US/10/282,048
CURRENT FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.6%;
Matches 251; Conservative
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                                                                                                                                                                                            ; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-10-282-048-2
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ORGANISM: Mus musculus
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US-10-282-048-5
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                                                                                                                                                               ; Sequence 4, Application US/10282048; Sequence 4, Application US/10282048; Sequence 4, Application US/10282048; Patent No. 6692948; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.; APPLICANT: WEI, Ming-Hui et al.; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: THEREOF; TITLE OF INVENTION: THEREOF; TITLE OF INVENTION: THEREOF; TITLE OF INVENTION NUMBER: US/10/282,048; CURRENT FILING DATE: 2002-10-29; NUMBER OF SEQ ID NOS: 6; SOFTMARE: FasteSEQ for Windows Version 4.0; SEQ ID NO 4; LENGTH: 251
; TYPE: PRT
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US-09-916-204-5
; Sequence 5. Application US/09916204
; Patent No. 663045
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01164CIP
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 201-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASESEQ for Windows Version 4.0
; SEQ ID NO 5
LENGTH: 251
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DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                 DLLSLINRYEDQLDENMIQPYLAELILAVHSVHQMGYVHRDIKPENILIDRYGHIKLVDF
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Best Local Similarity 90.4%
Matches 227; Conservative
                                                                 GSAAKMINSNKM 251
                                                                                              241 GSAAKWINSNKV 251
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ORGANISM: Mus musculus
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US-10-282-048-4
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RESULT 12
US-09-916-204-6
; Sequence 6, 38plication US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REPERENCE: C1001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastsEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 251
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                                                                                       1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
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  Length 251;
                                           Indels
Query Match
45.2%; Score 1177; DB 4;
Best Local Similarity 90.0%; Pred. No. 2.4e-105;
Matches 226; Conservative 16; Mismatches 9;
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## Sequence 8511, Application US/09949016
## Patent No. 6812339
## Sequence 8511, Application US/09949016
## Patent No. 681239
## Sequence 8511, Application US/09949016
## Sequence 8511, Application
## Sequence 8511, Application
## Sequence 8511, Application
## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
## TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
## CURRENT APPLICATION NUMBER: US/09/949,016
## PRIOR PRILING DATE: 2000-10-20
## PRIOR PILING DATE: 2000-10-03
## PRIOR PILI
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        ECSOPALMKMKHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG 120
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                                                                                                                                                                     DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
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US-09-949-016-8511
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Patent No. 6652948

GENERAL INFORMATION:
APPLICANT: WET, Ming-Hui et al.
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REPERENCE: CLOO1164CIP-DIV
CURRENT APPLICATION NUMBER: US/10/282,048
CURRENT PAILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FasteSEQ for Windows Version 4.0
SEQ ID NO 6
ILENGTH: 251
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Sequence 5, Application US/10282048

Patent No. 662948

GENERAL INFORMATION:
APPLICANT: WEL, MING-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, ITILE OF INVENTION: THEREOF
FILE REFERENCE: CL001164CIP-DIV
CURRENT APPLICATION NUMBER: US/10/282,048
CURRENT FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.
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90.0%; Pred. No. 2.4e-105;
tive 16; Mismatches 9;
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PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 2027 AA; 231429 MW; 6B1D8C3F661F357B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Citron Rho-interacting kinase short form.
Memo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001668; P:protein amino acid phosphorylation; IEA.
InterPro; IPR001099; Kinase like.
InterPro; IPR000961; Pkinase.
InterPro; IPR0002290; Ser_thr_pkinase.
InterPro; IPR001249; Tyr_pkinase.
InterPro; IPR001249; Tyr_pkinase.
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FORMAL PR001245; Tyr_pkinase.
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Mao Y., Xie Y., Wu Q.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
BBBL; AY209000; AAP43922.1; -.
HSSP; P05132; LATP.
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Pred. No. 5.7e-153;
2; Mismatches 0;
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                                                                     Best Local Similarity 99.6
Matches 466, Conservative
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-I. SIMILARITY: Belongs to the Ser/Thr protein kinase family.

-I. SIMILARITY: Belongs to the Ser/Thr protein kinase family.

HSSP: P31751; IMRV.

MGD; MG1:1051; IMRV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIKFKYGARNPSDAGAAEPIASRASRINLFFQGKPPFMTQQQMSPLSREGILDALLVLFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYLHRDIKPENILVDRTGHIKLVDF
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ProDom; PD000001; Prot_Kinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00130; TYKK; 1.

SMART; SM00131; TYKK; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE Dom; 1.

PROSITE; PS00108; PROTEIN KINASE Dom; 1.

ATP-binding; Kinase; Serime/threomine-protein kinase; Transferase.

SEQUENCE 482 AA; 54353 MW; 4F02AF6A32C73BAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99009084; PubMed=9792683; DOI=10.1074/jbc.273.45.29706;
DI CUNIO F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.
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                                                                                                                                                                                                                                                                                                                                                              Query Match 93.2%; Score 2425; DB 2; Length 482; Best Local Similarity 98.9%; Pred. No. 9.2e-153; Matches 463; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
NAM-2014 (TrEMBLrel. 26, Last annotation update)
NAM-2014: Synonyms-Criton kinase short isoform.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z
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M HSSP; P31/10; Intex.

M MG9; MGG:0005622; C:intracellular; IEA.

M MG9; GO:0005622; C:intracellular; IEA.

M G0; GO:0005624; F:APP binding; IEA.

M G0; GO:0005634; F:APP binding; IEA.

M G0; GO:0005634; F:Brotein serine/threonine kinase activity; IEA.

M G0; GO:0005643; F:Brotein serine/threonine kinase activity; IEA.

M G0; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.

M G0; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.

M G0; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.

M G0; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.

M G0; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.

M G0; GO:0005464; F:protein acid phosphorylation; IEA.

M M InterPro; IPR001809; Citron.

M InterPro; IPR001809; Minase C.

M InterPro; IPR000861; PRIM repeat.

M InterPro; IPR001809; Minase.

M InterPro; IPR001809; Minase; I.

M Ffam; PF00180; PRIMASE; I.

M Pfam; PF00180; PRIMASE; I.

M Pfam; PF00180; PRIMASE; I.

M Pfam; PF00180; PRIMASE; I.

M PRIMR; PR00180; PROPMYOSIN.

M PRIMR; PR000001; Prot Kinase; I.

M RANAT: SM00109; C1; I.
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                                                                                                                  MEDLINE-99009084; PubMed-9792683; DOI=10.1074/jbc.273.45.29706;
Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.
Dotto G.P.;
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R SMART; SM00109; CN1; 1.

R SMART; SM00123; PH; 1.

R SMART; SM00123; PH; 1.

R SMART; SM00123; FKC; 1.

R SMART; SM00123; S TKC; 1.

R PROSITE; PS00409; DAG PE BIND DOM 1; 1.

R PROSITE; PS50003; PH DOMAIN; T.

R PROSITE; PS50010; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS01009; PROTEIN KINASE ATP; 1.
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Best Local Similarity 88.0
Matches 412; Conservative
               NCBI_TaxID=10090;
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GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO: GO:0016469; P:protein serine/threonine kinase activity; IEA.

R GO; GO:0016468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR01009; Kinase_like.

R InterPro; IPR00051; Prot_kinase_C.

R InterPro; IPR000519; Prot_kinase.

R InterPro; IPR000519; Prot_kinase.

R InterPro; IPR000519; Prot_kinase.

R Pfan; PF000433; Pkinase.

R Pfan; PF000433; Pkinase.

R SMART; SM00133; PROT_Kinase; 1.

R SMART; SM00133; ZTK X; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS0011; PROTEIN KINASE ATP; 1.

R PROSITE; PS0011; PROTEIN KINASE ATP; 1.

R PROSITE; PS0011; PROTEIN KINASE ST; 1.

R ATP-binding; Kinase; Serine(threonine-protein kinase; Transferase.

SEQUENCE 494 AA; 55742 MW; 2C60D2294B28A185 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.3%; Score 2271.5; DB 2
Best Local Similarity 87.3%; Pred. No. 1.5e-142;
Matches 432; Conservative 27; Mismatches 35;
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Rho/rac-interacting citron Kinase.
Name-cit; Synonyme=Crik;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILPSVYAKGSARGRC 495
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Riausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosak S.A., McKernan R.J., McKernan R.J., Malank J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfaud G.G.,
Radresley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                     241 GSAAKWINSNKWVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
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                               DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                                           GSAAKMISIKKWYNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300
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                                                                                          GSAAKMISIK-VDAKLPIGTPDYMAPEVLTVMNEDRRGTYGLDCDWWSVGVVAYEMVYGK
                                                                                                                                                                                                                   TPFTEGTSARTFNNIMNFQRFLKRPDDPKVSSELLDLLQSLLCVQKERLKFEGLCCHPFF
                                                                                                                                                                                                                                                                                                                                         natural visualizativi Belongs to the Ser/Thr protein kinase family.

-1-SIMILARITY: Belongs to the Ser/Thr protein kinase family.

RHSSP; 231751; JMRV.

RGO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

RGO; GO:0006468; P:protein serine/threonine kinase activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00091; Protein acid phosphorylation; IEA.

R InterPro; IPR000919; Prot kinase.

R InterPro; IPR000919; Prot kinase.

R PROSITE; PRO00001; Prot kinase; 1.

R PROSITE; PRO0107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00117; PROTEIN KINASE ATP; 1.

R PROSITE; PS00117; PROTEIN KINASE EDO; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                 SPFAEGTSARTFINIIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF
                                                                                                                                                                                                                                                                                                    SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGEELPFVGFS
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Madaule P., Eda M., Watanabe N., Fujisawa K., Matsuoka T., Bito
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"Role of Citron kinase as a target of the small GTPase Rho
                                                                                                                                                                                                                                                                                                                                                                                                                          YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV
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90.9%; Pred. No. 4.8e-135;
ive 21; Mismatches 19; Indels
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Last annotation update)
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Best Local Similarity 90.9'
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Myotonic dystrophy kinase-related CDC42-binding kinase gamma
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Best Local Similarity 43.8%
Matches 184; Conservative
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=9606;
  SO COCCE TO THE SOURCE OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 RASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFV---RK 79
                                                                                                                                                                 ----ALGILGRSESVVSGLDSPAKTSSMEKKL-----LIKSKELQDS 461
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ted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
MILARITY: Belongs to the Ser/Thr protein kinase family.
BCO41741; AAH41741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.7%; Score 929; DB 2; Length 717; 41.7%; Pred. No. 3.1e-53; Live 84; Mismatches 148; Indels
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SEQUENCE
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R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

R GO; GO:0005083; F:small GTPase regulatory/interacting protein...;

GO; GO:00057242; P:intracellular signaling cascade; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR001180; Citron.

R InterPro; IPR001219; DAG PE-bind.

R InterPro; IPR001849; PH.

InterPro; IPR001849; PH.

InterPro; IPR001849; PH.

InterPro; IPR00195; Prote kinase.

R InterPro; IPR001209; Ser_chr_pkinase.

R InterPro; IPR001219; Prote kinase.

R InterPro; IPR001219; Tyr_tkinase.

R InterPro; IPR001219; Tyr_tkinase.

R InterPro; IPR001219; Tyr_tkinase.

R Pfam; PF00180; PBD; 1.

R Pfam; PF00180; PBD; 1.

R Pfam; PF00180; PBD; 1.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          Ng Y., Tan I., Lim L., Leung T.;
Submitted (UNN-2004) to the BMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- SIMILARITY: Contains 1 PH domain.
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43.8%; Pred. No. 8.2e-53;
ative 83; Mismatches 125; Indels 28
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RLKFEGL---CCHPFFSKIDWNNIRNSPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQL 404
                                                             379 PPPSHGAFSGHHLDFVGFTYT----SGSHSPESSSEAWAALERKLOCLEOE
                                                                                                    405 SP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTS----SMEKKLLIKSKE
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MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
                                                                                                                                                                                                                                                                                                                     Pterygota;
                                                                                                                                                                                                                                                                                                                            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR.2004 (TrEMBLrel. 26,
CG10522-PA.
ORFNames=CG10522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=22426069; PubMed=12537572; Misters S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Misters S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettenourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Filishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SM00120; STRC; 1.

PROSITE; PS50081; DAG PE BIND DOM 2; 1.

PROSITE; PS50011; DAG PE BIND DOM 2; 1.

PROSITE; PS50011; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine, Kinase; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Annotation of the Drosophila melanogaster euchromatic genome:
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-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AE003541; AAF49907.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Maninker J.S., Bergman C.M., Kronmiller B., Carlson J., Sv Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.4%; Score 922; DB 2; Length 18 40.1%; Pred. No. 3e-52; ive 99; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                          Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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                                                                                                                                                                                                                                           melanogaster euchromatic genome sequence."
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InterPro; IPR001180; Citron.
InterPro; IPR001180; Citron.
InterPro; IPR001219; DAG_PB-bind.
InterPro; IPR001019; Kinase like.
InterPro; IPR000961; Prinase C.
InterPro; IPR000919; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
Pfam; PF00069; CNH; I.
Pfam; PF00069; Pkinase; I.
Pfam; PF00069; CNH; I.
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373 PEDISNFDVDVCED--DFTPCLQETQPPRVLAAFTGNHLPFVGFSYTHG-SLLSDARSLT 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 AVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPE 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 P---KUSSDFLDLIQSLLCGQKERLKFEGLC---CHPFFSKIDWNNIRNSPPFFVPTLKS 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 DDDTSNFDEPEKNSWVSSSPC--QLSP----SGFSGEELPFVGFSYSKALGILGRSESVV 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 NIYMDG-----PSKKYPEALSFETLIDSLICLYDECCNSTLRKEKCIAEFVESVKTVISKA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 ILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 BIDWVVSEEAKDLIRQLICSSDVRFGRNGLSDFQLHPFFEGIDWNTIRDSNPPYVPEVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 NLFFQGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAEL
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                                                                                               Wormbase; WBGene00006437; K08B12.5.
Wormbase; WBGene00006437; K08B12.5.
Wormbase; K08B12.5; CE30B18.
GO; GO:0005674; F:Protein serine/threonine kinase activity; IEA.
GO; GO:0005083; F:small Grapae regulatory/interacting protein. .
GO; GO:0007422; P:intracellular signaling cascade; IEA.
GO; GO:0007422; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                                                  R InterPro; IPR001180; Citron.
R InterPro; IPR001219; DAG_PE-bind.
R InterPro; IPR001180; Citron.
R InterPro; IPR001180; Citron.
R InterPro; IPR0010180; Kinase like.
InterPro; IPR001099; Kinase like.
R InterPro; IPR000951; Pkinase C.
InterPro; IPR000951; Pkinase C.
InterPro; IPR000951; Pkinase C.
InterPro; IPR000951; Prot kinase.
R InterPro; IPR008271; Ser_thr_Dkin_AS.
R EnterPro; IPR008271; Ser_thr_Dkin_AS.
R Ffam; PF00169; Ph; 1.
R Ffam; PF00169; Ph; 1.
R Ffam; PF00169; Ph; 1.
R SMART; SM00199; CI; 1.
R SMART; SM00199; CI; 1.
R SMART; SM001285; Ph; 1.
R SMART; SM001285; Ph; 1.
R SMART; SM0013; S-TKC; 1.
R SMART; SM0013; S-TKC; 1.
R R SMART; SM0013; S-TKC; 1.
R R SMART; SM0013; Ph; 1.
R R SMART; SM0013; Fr; 1.
R R SMART; SM013; Fr; 1.
R R SMART; R SM013; Fr; 1.
R R SMA
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-!- SIMILARITY: Contains 1 PH domain.
                          EMBL; U97001; AAB52260.3;
PIR; T25808; T25808.
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                                                                                                                                                                                                                                                       SMGIIGYELICETTPPHEDNVHETYSKILSHCEESHLKELISFPADLKVSVNYRNLIESL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVOVVREKATGDIYAMKVMKKKKALLAQEQVSFPEEERNILSRSTSPWIPQLQYAFQDKNH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                 342 LCGQKERLKFEGLCCHPFFSKIDWNIRNSPPFFVPTLKSDDDTSNFDE-----PEKN 394
                                               395 SWVSSSPCQLSPSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIK 454
                                                                                                                                                     LYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILV
                                                                                                                                                                                                                            DRTGHIKLVDFGSAAKMNSNKMYNAKLPIGTPDYMAPEVLTVMNGD--GKGTYGLDCDWW
                                                                                                                                                                                                                                                                                                                               SVGVIAYEMIYGRSPFAEGTSARTFNNIM-----NFQRFLKFPDDPKVSSDFLDLIQSL
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wormbase Consortium;
"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 28:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Bristol N2;
WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
Becker M., Wohldmann P.;
"The sequence of C. elegans cosmid KOBB12.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Temporarily assigned gene name protein 59.
Name-tag-59, ORFNames-K08B12.5,
Caenorhabditis elegans.
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MEDLINE=99069613; PubMed=9851916;
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Submitted (AUG-2003)
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SMART; SM0020; STKC; 1.
SMART; SM00103; STKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                     Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000664P; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the Ser/Thr protein kinase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Eye;
Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56805 MW; 5F9FBD9CC1D2AEFC CRC64;
                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                            492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001009; Kinase_like.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR00019; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
Pfam; PP00069; Pkinase; I
                                                                                                                                                                                                         Created)
                                                                                                                                                            PRT;
                            430 DEIRAIAQRCQGDAELMEKS 449
436 SGLDSPAKTSSMEKKLLIKS
                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, oll-MR-2004 (TrEMBLrel. 26, CDC42BPB protein (Fragment). Name=CDC42BPB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to t
EMBL; BC048261; AAH48261.1;
HSSP; P31751; 1MRY.
                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 AA;
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                                                                                                           RESULT 10

086XZ8

10 66XZ

AC 086XZ

AC 086XZ

DT 01-MA

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Score 896.5; DB 2; Length 492; Pred. No. 2.8e-51;

34.5%;

Query Match Best Local Similarity

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MEDLINE-EPITIONEN SYSTEM;

MEDLINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUSPECT R.L., Feingold R.A., Grouse L.H., Derge J.G.,

MAISCHOL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHOL S.F., Jordan H., Moore T., Max S.I., Wang J., Halpe F.,

MA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

METARUSPECT M.J., Modin T.B., Toshiyuki S., Carninol P., Prange C.,

METARUSPECT M.J., McEwnan R.J., Malek J.A., Gunaratne P.H.,

MISCHOL S., Wolfur D.M., Sodergen B.J., Lu X., Gibbs R.A.,

MISCHOL B., Kutreman M., Sodergen B.J., Lu X., Gibbs R.A.,

MILIALON D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

MILIALON B., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MILITING M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

MA Rakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

MA Rakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

MA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butrerfield Y.S.,

MA JONES S.J., Marra M.A.,

MA JONES M. M. SONO Full-length human
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                                                                                                                                                                                                                   143 FQDENHLYLVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 202
                                                           44 SPLSREGILDALFVLFEECSOPALMKIKHVSNFVRKYSDTIAELOELOPSAKDFEVRSLV 103
                                                                                                                                                                                 104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSFWIPQLQYA 163
                                                                                                                                                                                                                                                                                                164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                       PENILVDRTGHIKLVDFGSAAKMISNKWYNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEERFQFPSHVTDVSEEAKDLIQRLI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :: || || : : || || 322 CSRERRIGQNGIEDFKKHAFFEGINWENIRNIEAPYIPDVSSPSDTSNFDVDDDVLRNTE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 I-----LPPGSHTGFSGLHLPPIGFTFT------TESCFS--DRGSLKSIMQSNTLT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 CGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPFVPTLKSDDDTSNFDEPE---KNSW 396
                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 SALSVETLLDVLVCLYTECSHSALRRDKYVABFLEWAKPFTQLVKEMQLHREDPELIKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 VSSSPCQLSP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI
29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   85; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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U-JUN-2004 (TrEMBLrel. 26, Last annotation update)
CDC4-2BB protein (Fragment).
Name=CDC42BB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               933 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :::| :| | : : |
426 KDEDVQ--RDLEHSLQMEA 442
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   Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                       224
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143 FQDENHLYLVMDYYVGGDLLTLLSKFEDKLPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 PENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 SALSVETLÍDVLVCLYTEČSHSALRRDKÝVABFLEWAKPFTQLVKÉMÓLHREDFEIIKVI
                                                                                                                                                                                                                 MEDLINE=99216425; PubMed=10198171; DOI=10.1006/geno.1999.5769;
Moncrieff C.L., Bailey M.E., Morrison N., Johnson K.J.;
"Cloning and chromosomal localization of human Cdc42-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding, Kinase, Serine/threonine-protein kinase, Transferase
SEQUENCE 1711 AA; 194356 MW; 3A3731D40A363497 CRC64;
                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:000585; C:cytoskeleton; TAS.
GO; GO:0004672; F:protein kinase activity; TAS.
GO; GO:0004672; F:protein kinase activity; TAS.
GO; GO:0007165; P:stablishment and/or maintenance of cell po.
GO; GO:0007165; P:stagnal transduction; TAS.
InterPro; IPR001219; DAG_PE-bind.
InterPro; IPR011009; Kinase like.
InterPro; IPR000095; PAKbox/Rhobndng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1711;
                                                                                                                                                                                                                                                                                                                              Genomics 57:297-300(1999).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AF128625; AAD37506.1; -.
HSSP; P31751; 1MR7.
                         Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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34.5%; Score 896.5; DB 2;
Best Local Similarity 42.1%; Pred. No. 1.3e-50;
Matches 185; Conservative 85; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00479; DAG PE BIND DOM 1; 1.
PROSITE; PS50081; DAG PE BIND DOM 2; 1.
PROSITE; PS50003; PH DOMAIN; 1.
PROSITE; PS500107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR011009; Kinase like.
InterPro; IPR000095; PAKbox/Rhobndng.
InterPro; IPR0001849; PH.
InterPro; IPR0001961; Pkinase C.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008210; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00109; C1; 1.
SMART; SM00036; CNH; 1.
SMART; SM00285; PBD; 1.
SMART; SM00233; PH; 1.
SMART; SM00220; S TKC; 1.
SMART; SM00133; S TKC; 1.
PROSITE; PS50108; CRIE; 1.
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                          kinase beta.";
                                                                                                                                                                                                TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PODKOWILYLVMEYOPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 FQDENHLYLVMDYYVGGDLITLLSKREDKIPEDMARFYIGEMVLAIDSIHQLHYVHRDIK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENILVDRIGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGOKERLKFEGL---CCHPFFSKIDWNNIRNSPPFFVPTLKSDDDTSNFDEPE---KNSW 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 I-----LPPGSHTGFSGLHLPFIGFTFT----TESCFS--DRGSLKSIMOSNTLT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSRERRIGGNGIEDFKKHAFFEGLNWENIRNLEAPYIPDVSSPSDTSNFDVDDDVLRNTE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 VSSSPCQLSP---SGPSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 SALSVETLLDVLVCLYTECSHSALRRDKYVAEFLEWARPFTQLVKEMQLHREDFEIIKVI
                                                                                                                                                                            R GO; GO:0005524; F:protein serine/threonine kinase activity; IEA.

GO; GO:0005524; F:protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F:protein serine/threonine kinase activity; IEA.

GO; GO:0016468; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR000969; Kinase_like.

R InterPro; IPR00019; Prot kinase.

R InterPro; IPR00199; Prot kinase.

R InterPro; IPR00199; Prot kinase.

R PROMON; PROMON; Prot kinase.

R PROMON; PROMON; Prot kinase; 1.

SMART; SMO013; STK; 1.

R SMART; SMO013; STK; 1.

R PROSITE; PSO010; PROTEIN KINASE ATP; 1.

R PROSITE; PSO010; PROTEIN KINASE DOM; 1.

R PROSITE; PSO010; PROTEIN KINASE DOM; 1.

R ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.5%; Score 896.5; DB 2; Length 933; 42.1%; Pred. No. 6.2e-51; tive 85; Mismatches 140; Indels 29
                    TISSUE-Peripheral Nervous System;
Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BC047871; AA447871.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         933 AA; 108543 MW; 38E7179C3253F521 CRC64;
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Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last se
01-NOV-1999 (TrEMBLrel. 12, Last se
01-MAR-2004 (TrEMBLrel. 26, Last ar
CDC42-binding protein kinase beta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454 KSKELQDSQDKCHKVFISA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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SEOUENCE
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Q9Y5S2
ID Q9Y5S;
AC Q9Y5S;
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-NO
Service Services Serv
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                                                                                                                                                                                          382 I-----LPPGSHTGFSGLHLPPIGFTFT------TESCFS--DRGSLKSIMQSNTLT 425
CDWWSLGVCMYEMLYGETPFYAESLVETYGKIMNHEBRRQFPSHVTDVSEEAKDLIQRLI 321
                                                                     CGOKERLKFEGL---CCHPFFSKIDWNNIRNSPPFFVPTLKSDDDTSNFDEPE---KNSW 396
                                                                                                  397 VSSSPCQLSP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R HSSP; P31751; JRKY.

R Genew, HGMC:1738; CDC42BPB.

GO; GO:00064674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0007242; F:small GTPase regulatory/interacting protein. .;

GO; GO:0007242; F:small GTPase activity; IEA.

GO; GO:0007242; P:intracellular signaling cascade; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; IEA.

R InterPro; IPR001219; DG, Pe-bind.

R InterPro; IPR001099; Kinase like.

R InterPro; IPR001099; Kinase like.

R InterPro; IPR00199; PH:nase C.

R InterPro; IPR00199; PH:nase C.

R InterPro; IPR001919; Prot kinase.

R InterPro; IPR001919; Prot kinase.

R InterPro; IPR001919; Prot kinase.

R InterPro; IPR001919; Ext. kinase.

R Pfeam; PF001190; Gr. Lir. pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAA1124 protein (Fragment).
Name=KIAA1124;
Home sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1760 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD000001; Prot kinase; 1.
SWART; SW00109; C1; 1.
SWART; SW00036; CNH; 1.
SWART; SW00235; PBD; 1.
SWART; SW00233; PH; 1.
SWART; SW00123; STKC; 1.
SWART; SW00133; STKC; 1.
PROSITE; PSS0108; CREB; 1.
PROSITE; PSS0108; CREB; 1.
                                                                                                                                                                                                                                                        454 KSKELQDSQDKCHKVFISA 472
                                                                                                                                                                                                                                                                                   | :::| :| : |
KDEDVQ--RDLEHSLQMEA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00069; Pkinase, 1.
Pfam, PF00433; Pkinase C, 1.
PRINTS; PR00008; DAGPEDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00780; CNH; 1
Pfam; PF00786; PBD; 1
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
Q9ULUS
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44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 SALSVETLLDVLVCLYTECSHSALRRDKYVAEFLEWAKPFTQLVKEMQLHREDFEIIKVI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 PQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 PENILVDRIGHIKLVDFGSAAKMISNKMYNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :: | | | | | : | | | | 371 CSRERRIGQNGIEDFKKKHAFFEGINWENIRNIEAPYIPDVSSPSDTSNFDVDDDVLRNTE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 CGQKERLKFEGL---CCHPFFSKIDWNIRNSPPPFVPTLKSDDDTSNFDEPE---KNSW 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 GCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 VSSSPCQLSP---SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLI
                                                                                                                                                                                                                                                                                                                                                                                                                  29; Gaps
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase...
SEQUENCE 1760 AA: 199200 ...
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
Interpro; IPR001009; Kinase_like.
InterPro; IPR000051; Pkinase_C.
InterPro; IPR000219; Prot_kinase.
InterPro; IPR0002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Figm; PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                  Length 1760;
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Zhao Y., Kidd V., Kraft A.S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; US9305; AAB37126.1; -.
HSSP; P31751; 1MRY.
                                                                                                                                                                                                                                                                                                                                              Query Match 34.5%; Score 896.5; DB 2; Length Best Local Similarity 42.1%; Pred. No. 1.4e-50; Matches 185; Conservative 85; Mismatches 140; Indels
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Homo sapiens (Human).
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F:small GTPase regulatory/interacting protein.
                                                                                                                                                                                                                        Pfam, Pro0069; Pkinase; 1.
Pfam; Pro0069; Pkinase C; 1.
PRINTS; PRO0009; DAGPEDOMAIN.
PRODOM; PROSTES; PSS0109; CRIB; 1.
PROSITE; PSS01047; DAG PE BIND DOM 1; 1.
PROSITE; PSS00081; DAG PE BIND DOM 2; 1.
PROSITE; PSS00081; PROFEIN KINASE ATP; 1.
PROSITE; PSS01011; PROTEIN KINASE ATP; 1.
PROSITE; PSS01011; PROTEIN KINASE DOM; 1.
PROSITE; PSS01011; PROTEIN KINASE DOM; 1.
                                                           InterPro; IPR001180; Citton.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR001009; Kinase_like.
InterPro; IPR001099; PAKbox/Rhobndng.
InterPro; IPR001849; PH.
InterPro; IPR000719; Prot kinase_C.
InterPro; IPR000719; Prot kinase.
InterPro; IPR00871; Ser_thr_pkin_AS.
Pfam; PP00130; Cl 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 KORLSPDSTRKĽÓD 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.03
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       1573
                                                                                                                                                                                                              PF00169; PH; 1.
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Job time : 179
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SEQUENCE
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                                                                                                                                                                                                                                                                     DFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSF 155
                                                                                                                                                                                                                                                                                                                               WIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQPYLAELILAVHSVHLM 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| || :|||||:|| |||:|| ||| :|| || GKGRYGPECDWWSLGVCMYEMLYGSTPFYAESLVETYGKIMMHKERFQFPAQVTDVSENA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDF 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDLIQSLLCGQKERLKFEGL---CCHPFFSKIDWNNIRNSPPFVPTLKSDDDTSNFDEP 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDCLKNSETMPPP---THTAFSGHHLPFVGFTYTSSCVLSDRSCLRVTAGPTSLDLDVNV 431
                                                                                                                                                                                                                                          75
                                                                                                                                                                                                           36 PFWTQQQMSPLSREGILDALFVLPBECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAK 95
                                                                                                                                                                                                                              PAQTNGQY--FSVETLLDILICLYDECNNSPLRREKNILEYLEWAKPFTSKVKQMRLHRE
                                                                                                                                                                                                                                                                                                                                                                                                        GYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E---KNSWVSSSPCQLSPSGFSGEELPFVGFSYSKALGILGRS------ESV
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
Pfam; PP00433; Pkinase_C; 1.
ProDom; PD00001; Prot_kinase; 1.
SWART; SW00220; 2_TKc; 1.
SWART; SW00137; 5_TKc; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serime/threonine-protein kinase; Transferase.
SRQUENCE 496 AA; 56991 MW; 069186D74AE9C936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.

EMBL, AAABO108986; EAAO1280.2; -.

HSSP, P31751; IMRV.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles Genome Sequencing Consortium,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
--- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                   Length 496;
                                                                                                                                                  34.2%; Score 891; DB 2; Length 496
40.3%; Pred. No. 6.5e-51;
ive 92; Mismatches 145; Indels
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Last annotation update)
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01-MAR-2004 (TrEMBLrel. 26, C.
01-MAR-2004 (TrEMBLrel. 26, L.
01-MAR-2004 (TrEMBLrel. 26, L.
ENSANGPO000009214 (Fragment)
                                                                                                                                                                 Local Similarity 40.3% tes 183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 NILVDRTGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCD
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GO:0005083; F:small GrPase regulatory/interacting prot GO:0016740; F:transferase activity; IEA. GO:0007242; P:intracellular signaling cascade; IEA. GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 891; DB 2; Length 15; Pred. No. 2.8e-50; 90; Mismatches 146; Indels
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

US-10-724-594-2 2602 1 MLKFKYGARNPLDAGAAEPI.......CSRILPSVYAKGSARGRCWL 497 Title: Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		o)p			SUMMARIES	
Result No.	Score	Query Match	Length	DB		Description
	908.5	34.9	1548	7	T25808	hypothetical prote
8	891	34.2	1732	~	T14039	protein kinase (EC
e	883	33.9	1702	7	T14050	
4	876.5	33.7	1173	7	T25539	Ñ
S	866.5	33.3	1354	7	S74244	serine/threonine-s
9	864.5	33.2	1354	~	S69211	serine/threonine-s
7	863	33.2	624	7	B49364	protein kinase (EC
80	860.5	33.1	1388	7	S70633	serine/threonine-s
6	853.5	32.8	1388	7	S74245	serine/threonine-s
10	847	32.6	557	~	S71829	serine/threonine-s
11	721	27.7	522	~	G86431	protein kinase TSI
12	711	27.3	479	~	S42864	protein kinase (EC
13	704	27.1	756	~	996098	probable protein k
14	701	26.9	526	~	S49077	protein kinase PKT
15	700	26.9	469	~	T41723	serine/threonine-s
16	697	26.8	296	~	F84589	probable protein k
17	693	26.6	569	7	A86170	hypothetical prote
18	687.5	26.4	474	7	178396	myotonic dystrophy
19	685	26.3	441	~	178393	myotonic dystrophy
20	685	26.3		7	178394	myotonic dystrophy
21	682.5	26.2	-	7	T16718	hypothetical prote
22	676.5	26.0		~	D71405	probable protein k
23	676.5	26.0		~	H85156	protein kinase (im
24	674.5	25.9	465	7	138133	kinase (
25	665.5	25.6		~	S42867	kinase (
26	6.099	25.4	483	N	T05188	protein kinase F4I
27	639	24.6	ß	~	T01288	protein kinase F27
28	636.5	24.5	598	~	T47254	serine/threonine k
29	636.5	24.5	665	7	S70706	probable protein k

382 DDDTSNFDEPEKNSWVSSSPCQLSP----SGFSGEELPFVGFSYSKALGILGRSESVVSG 437

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328 P---KVSSDFLDLIQSLLCGQKERLKFEGLC---CHPFFSKIDWNNIRNSPPFFVPTLKS 381

serine/threonine k	probable protein k	hypothetical prote	myotonic dystrophy	tumor suppressor p	probable serine/th	probable serine-th	protein kinase DBF	protein kinase DBF	probable protein k	protein F27F5.23 [	hypothetical prote	protein kinase (EC	probable serine/th	protein kinase (EC	probable prolifera
T47255	S22711	T25035	178395	A56155	862556	T41341	859776	S64387	S22258	H96509	863378	S41099	T38171	T17287	T50414
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636	636	608	606.5	604	548	536	532.5	522	520.5	520	516	515	510.5	210	509

## ALIGNMENTS

RESULT 1	
T25808	Second of the se
C:Species: Cae	ypourectical pictoria. C.Species: Caenorhabditis elegans
C; Date: 15-Oct	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
C, Accession: T	255808
K; Becker, M.; Wonldmann, P.	Kibecker, M.; Wohldmahn, P. suhmitted to the EMBI Data Library annil 1907
A;Description:	becarring to the sequence of C. elegans cosmid KOBB12.
A; Reference number:	imber: Z20091
A;Accession: T25808	2.25808
A; Scatus: preliminar A: Molecule type: DNA	Ajsterus: preliminary; cranstated from Gb/Bmbb/UDBu Ajsterule type: DNA
A, Residues: 1-1548 <bec></bec>	.1548 <bec></bec>
A, Cross-refere	A;Cross-references: UNIPROT:001583; EMBL:U97001; PIDN:AAB52260.1; GSPDB:GN00023; CESP:KOr A.Exnerimental source: strain Bristol NO: clone KORR12
C:Genetics:	
A; Gene: CESP: K08B12.5	(08B12.5
A; Map position: 5	1: 5 1: 66/1: 156/3: 278/2: 201/2: 620/1: 1022/2: 1273/3: 1226/1: 1423/2: 1400/:
C.Superfamily.	Allittoins: Joy II God'II 1201/11 1201/12 JOY 200/II 1044/4; 141/5/5 1340/II 1442/4; 1403/4 C.Sunderfamillo: profesi kinasa homologu
F;956-1005/Dom	C. orpertaming, process Armade momentagy repeat homology <kzn></kzn>
Query Match	34.9%; Score 908.5; DB 2; Length 1548;
Matches 178	best Local Similarity 40.5%; Fred. No. 2.35-33; Matches 178; Conservative 91; Mismatches 150; Indels 19; Gaps 7;
Ωγ 28	NLFFOGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTJAEL 87
. da	
δλ	QELQPSAKDPEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSPFBEBRN 147
Db 74	
Qy 148	ILSRSTSPWIPQLQYARQDKNHLYLVWEYQPGGDLLSLLNRYEDQLDENLIQFYLAELIL 207
Db 134	:
Qy 208	AVHSVHIMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKAVNAKLPIGTPDYMAPE 267
Db 194	:  :  :
Qy 268	VLTWANGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD 327
Db 254	:      :     :     :    :     :

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R;Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L. Mol. Cell. Biol. 18, 130-140, 1998
A;Title: Myotonic dystrophy kinase-related Cdc42-binding A;Reference number: Z17862; WUID:98078670; PMID:9418861 A;Accession: T14050
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Matches 182; Conservative
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A;Gene: CESP:C10H11.9
A;Map position: 1
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protein kinase (EC 2.7.1.37) beta, myotonic dystrophy-associated - rat C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004 C;Accession: T14050
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAQTNGQC--FSVETLLDILICLYDECHNSPLRREKNILEYLEWAKPFTSKVKQMRLHRE
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K,Reywords: ATP; phosphotransferase
F;75-343/Domain: protein kinase homology «KIN»
F;1013-1062/Domain: protein kinase C zinc-binding repeat homology
                                                                                                                                                                                                                                                                                                                                                                                          34.2%; Score 891; DB 2; Length 1732; 40.3%; Pred. No. 1.5e-32; ive 91; Mismatches 146; Indels 3
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1702 <LEU7
A;Cross-treferences: UNIPROT:054875; EMBL:AF021936; NID:g2736152; PID:g2736153; PIDN:AACO:C;Genetics:
C;Genetics:
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: 1-1173 cDAN>
A,Residues: 1-1173 cDAN>
A,Cross-references: UNIPROT:P92199; EMBL:U88311; PIDN:AAB42348.1; GSPDB:GN00019; CESP:C10
A,Experimental source: strain Bristol N2; clone C10H11
effector
a Cdc42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 CDWWSLGVCMYEMLYGETPPYAESLVETYGKIMNHEBRRQFPSHVTDVSEBAKDLIQRLI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 CGOKERLKPEGL---CCHPFSKIDMNNIRNSPPFVPTLKSDDDTSNFDEPE---KNSW 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435
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C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 SPLSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 GRGAFGEVAVVKMKNTERIYAMKILNKWEMLKRAETACFREERDVLVNGDCQWITALHYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENILVDRIGHIKLVDFGSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDD-PKVSSDFLDLIQSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 VSSSPCQLSP---SGFSGEELPFVGFSYS-----KAL---GILGRSESVVSGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 I-----LPPGSHTGFSGLHLPFIGFTFTTESCFSDRGSLKSMIQSNTLTXDEDVQRDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 SSLSVETLLDVLVCLYTECSHSALRRDKYVAEFLEWAKPFTQLVKDMQLHREDFEIIKVI
kinase acts as
                                                                                                                                                                                                                                                                                                                          C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase
F;74-342/Domain: protein kinase homology <KIN>
F;1027-1076/Domain: protein kinase C zinc-binding repeat homology <KZN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.5%; Pred. No. 3.32
tive 90; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.9%; Score 883; DB 2; 40.5%; Pred. No. 3.4e-32;
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R;Dante, M.; Wansley, P.
submitted to the EMBL Data Library, February 1997
A;Description: The Sequence of C. elegans cosmid
A;Reference number: Z20047
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A;Accession: S69211
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1354 <ISH1.>
A;Residues: 1-1354 <ISH1.>
A;Cross-references: UNIPROT:Q13464; EMBL:U43195; NID:g1276900; PIDN:AAB02814.1; PID:g127
A;Accession: S71910
A;Accession: S71910
A;Residues: 187-195;281-288;465-473;573-587;818-828;885-893;934-945 <ISH2.>
C;Superfamily: protein kinase C zinc-binding repeat homology; protein kinase homology <ISH2.>
C;Superfamily: protein kinase homology <XIN.>
E;74-338/Domain: protein kinase ATP-binding motif
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <XZN.>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: S69211; S71910
R;Ishlizaki, T.; Mackawa, M.; Fujisawa, K.; Okawa, K.; Iwamatsu, A.; Fujita, A.; Watanabe EMBO J. 15, 1885-1893, 1996
A;Title: The small GTP-binding protein Rho binds to and activates a 160 kDa Ser/Thr prot A;Reference number: S69211; MUID:96203110; PMID:8617235
                                                                                                                                                                                                                                               378
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     CDWWSVGVFLYEMLVGDTPFYADSLVGTYSKIMNHKNSLTFPDDNDISKEAKNLICAFLT 318
                                                                                                                                                                                          344 GOKERLKFEG---LCCHPFFSKID--WNNIRNSPPFFVPTLKSDDDTSNFDEPEKNSWVS 398
                                                                                                                                                                                                                                                                                                    SS-PCQLSPSGFSGEELPFVGFSY----SKALGILGRSESVV--SGLDSPAKTSSME 448
                                                                                                                                                                                                                                                                                                                                  103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 PDNMLLDKSGHLKLADFGTCMKMNKEGMVRCDTAVGTPDYISPEVLKSQGGD--GYYGRE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 CDWWSVGVFLYEMLVGDTPFYADSLVGTYSKIMNHKNSLTFPDDNDISKEAKNLICAFLT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - human C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                         319 DREVRLGRNGVEEIKRHLFFKNDQWAWETLRDTVAPVVPDLSSDIDTSNFDDLEEDKGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PENILVDRTGHIKLVDFGSAAKMISNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLD
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Best Local S:
Matches 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scring/threonine-specific protein kinase (EC 2.7.1.-) isoform I, Rho-associated - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C; Accession: S74244
R; Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A; Title: ROCK-II, two isoforms of Rho-associated coiled-coil forming protein A; Reference number: S74244
A; Reference number: S74244
A; Reterence number: S74244
A; Residues: 1-1354 «NMLD: 95368048; FMID: 8772201
A; Molecule type: mRNA
A; Residues: 1-1354 «NMLS
A; Residues: 1-1354 «NMLS
A; Residues: UNIPROT: P70335; EMBL: U58512; NID: g1514695; PIDN: AAC53132.1; PID: g151
C; Superfamily: protein kinase homology
C; Keywords: coiled coil; phosphotransferase; serine/threonine-specific protein kinase
F; 74-338/Domain: protein kinase homology «KIN»
F; 1229-1283/Domain: protein kinase C zinc-binding repeat homology «KZN»
A;Introns: 23/3; 51/1; 104/3; 343/1; 478/2; 868/3; 891/3; 970/3; 1027/3; 1114/1
C;Superfamily: hypothetical protein C10H11.9; protein kinase homology
                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                 SPLSREGILDALFVLFEECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PENILVDRTGHIKLVDFGSAAKWNSNKMVNAKLPIGTPDYMAPEVLTVWNGDGKGTYGLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLC 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 GQKERL---KFEGLCCHPFFSKIDWN--NIRNSPPFVPTLKSDDDTSNFDEPEKNSWVS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 AAPDRIGENSVDDIRNHKFFVNDEWTPATLREASPPVIPSLKSDDDTTHFEEIETRDRDN 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163
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                                                                                                                                                                                                                                                                                                                                FODKNHLYLVMEYOPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIK 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 SSPCQLSPSGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEK 449
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                                                                                   Length 1173
                                                                                                                                     IndelB
                                                                             33.7%; Score 876.5; DB 2;
40.9%; Pred. No. 4.7e-32;
iive 88; Mismatches 142;
                                                                           Query Match
Best Local Similarity 40.9<sup>3</sup>
Matches 168; Conservative
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Scringly threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - bovine N; Alternate names: Rho-associated protein kinase (Species Bos primigentus taurus (cattle) (C;Species Bos primigentus taurus (cattle) (C;Accession: 170633; 877694 (Species 14-Pe-1997 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004 (C;Accession: 870633; 877694 (R;Matsui, T.; Amano, M.; Yamamoto, T.; Chihara, K.; Nakafuku, M.; Ito, M.; Nakano, T.; Oly R;Matsui, T.; Amano, M.; Yamamoto, T.; Chihara, K.; Nakafuku, M.; Ito, M.; Nakano, T.; Oly A;Reference number: 870633; MUID:96208507; PMID:8641286 (Rinase, as a putative target for A;Reference number: 870633; MUID:96208507; PMID:8641286 (Rinase, as a putative target for A;Residues: 1-1388 (AMIL) (Rinase, MIN) (Rinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 QLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNKM 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 YSKIMDHKNSLCFPEDAEISKHAKNLICAFLTDREVRIGRNGVEEIKQHPFFKNDQWNW 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: protein kinase C zinc-binding repeat homology; protein kinase P. C;Superfamily: phosphotransferase; serine/threonine-specific protein kinase E;90-354/Domain: protein kinase homology <KIN> F;90-354/Domain: protein kinase homology <KIN> F;98-106/Region: protein kinase Arb-binding motif F;1261-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>
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                                                                                                                                                                                                                                                                                                                                                     ::| | | ::| ::| ISDIREGAPLGVHLPFVGYSYS----CMALRDSEVPG---PTPMEVBAEQLLEPHVQAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 GQKERLKFEG---LCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSS
                                                                                                                                                                                                                  320 PPETRLGRGGAGDFRTHPFFFGLDWDGLRDSVPPFTPDFEGATDTCNFDLVEDGLTAMET
                                                                                                                                                                                                                                                                                                  401 PCQLSPSGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKIL---IKSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 VNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 FUNIMNPQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEG---LCCHPFFSKIDWN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 GAAEPIAN---RASRINLFFQGKPPFMTQQQMSPLSREGILDALFVLFEECSQPALMKIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQDS---QDKCHKVFISAA 473
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A; Status: preliminary
A; Molecule type: mRND
A; Residues: preliminary
A; Molecule type: mRND
A; Residues: 1-417, 'L', 419-468, 'P', 470-544, 'MAPRPWLWASARWWGOAPCTAATCCSLPGS', 'LGLAYRRRFPCS
A; Cross-references: GB:S72883; NID:g633864; PIDN:AAB31800.1; PID:g633865
A; Cross-references: GB:S72883; NID:g633864; PIDN:AAB31800.1; PID:g633865
A; Cross-references: GB:S72883; NID:g633864; PIDN:AAB31800.1; PID:g633865
A; Tibe: Molecular Day
A; Reference number: A4210.1
A; Molecular Day
A; Mole
                                                                                                                                                                                                                                                                                                                   RESULT 7
B49354
protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - human
NyAlternate names: myotonin protein kinase
C;Species: Homo sapiens (man)
C;Species: Myourisely, Myourisely, Harley, H.G.; Crow, S.R.; Sohn, R.; Thirion,
Genomics 18, 673-679, 1993
A;Title: Genomic organization and transcriptional units at the myotonic dystrophy locus.
A;Recession: B49364
A;Recession: B49364
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-624 <SHA
A;Residues: L-624 <SHA
A;Residues: UNIPROT:Q09013; GB:L19268; NID:g307176; PIDN:AAA36206.1; PID:g307177
R;Ssasgawa, N.; Sorimachi, H.; Maruyama, K.; Arahata, K.; Ishiura, S.; Suzuki, K.
FEBS Lett. 351, 22-26, 1994
A;Title: Expression of a novel human myotonin protein kinase (MtPK) CDNA clone which enc
379 ETFPI---PKAFVGNQLPFVGFTYYSNRRYLSSANPNDNRTSSNADKSLQESLQKTIYKL 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFF-DDPKVSSDFLDLIQSLLC 343
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Pred. No. 1e-31;
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C,Superfamily: protein kinase homology
C,Keywords: ATP; phosphotransferase
F,69-319/Domain: protein kinase homology «KIN»
F,77-85/Region: protein kinase ATP-binding motif
                                                                                                                              KE-----LODS-ODKC 465
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Best Local Similarity 40.8'
Matches 179; Conservative
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probable protein kinase YNL161w (EC 2.7.1..) - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypotherical protein N1727
C;Species: Saccharomyces cerevisian
C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 16-Aug-2004
C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 16-Aug-2004
C;Accession: S60966; S63113; S63813
R;Masr, F; Becam, A.M.; Herbert, C.J.
C,Accession: Simple Data Library, October 1995
A;Description: The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Argeterion: 186958
A.Reference number: 860958
A.Reference number: 860968
A.Reference number: 860968
A.Reference number: 860968
A.Residues: 1-756 <NAS>
A.Residues: 1-756 <NAS
A.R
                                                                                                                                                                                                                                                            336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 ADNSSQSTSKAGPWRKMLSSKDLNFVGYTY-KNPEIV--NDYQVPGIAELKKKDTKPKRP 428
                                                      276
                                                                                                                                                                                                  251
                                                                                                                                                                                                                                                                                                                                                                          337 LIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEK 393
                                                                                                                                                                                                                                                                                                                                                                                                           312 LISKLLCAVTQRLGSNGAHEIKLHPWFNGIDWERIYQMEAAFIPEVNDELDTQNFEKFEE 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 NSWVSSSPCQLSP--SGFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKL 451
                                                                                                                                                                                                                                                                                           252 KKGYGMECDWWSLGAIMYEMLVGYPPFYSDDPMSTCRKIVNWRTHLKPPEBAKLSPEAKD
                                                                                                                                         -----SNKMVNAKLPIGTPDYMAPEVLTVMNGDG
                                                                                                                                                                                                  198 FEVNNGNGGSPSNEGSTKPRRTQQEQLQHWQKNRRMLAYSTVGTPDYIAPEVLL----
                                                                                                                                                                                                                                                            KGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLD
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                              NLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMN
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A;Accession: S63813
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 307-756 <NAF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Superfamily: protein kinase homology C, Keywords: ATP; phosphotransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 LIKSKELQDSQD 463
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                           A,Cross-references: UNIPROT:095A79; GB:AE005172; NID:g4587520; PIDN:AAD25751.1; GSPDB:GR
Genetics:
A,Map position: 1
C,Superfamily: Arabidopsis thaliana protein kinase T518.9; protein kinase homology
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C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 06-Jan-1995 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: S42864
R;Baur, B.; Winter, K.; Fischer, K.; Dietz, K.
submitted to the EMBL Data Library, March 1994
A;Description: Molecular cloning and characterization of several protein kinases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEQVSFPEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNRYEDQLDE 195
                                                                                                                                                                                                                                                                                              69 KIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVM 128
                                                                                                                                                                                                                                                                                                                                                                                                           KKKALLAQEQVSFFEBERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLSLLNR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --NKMVNAKLPIGTPDYM 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 KNFPDFKAELVDRSTKPAAEHDRLSKPPSAPRRTQQEQLLHWQQNRRTLAFSTVGTPDYI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDDTSNFDEPEKNSWVSSSPCQLSPSG-----FSGEELPFVGFSYSKALGILGRSESVV 435
                                                                                                                                                                                                                                                                                                                               PDDPKVSSDFLDLIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPFFVPTLKS 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNS
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                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                             Length 522;
                                                                                                                                                                 27.7%; Score '**, 35.9%; Pred. No. 1.8e-25; ...ive 82; Mismatches 132; Indels ...ive
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Best Local Similarity 36.8%;
Matches 159; Conservative 7
                                                                                                                                                                                                     Best Local Similarity 35.9
Matches 158; Conservative
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A;Molecule type: mRNA
A;Residues: 1-479 <BAU>
      <STO
A;Residues: 1-522
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                                                                                                                                                                                Query Match
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Worm

C.E.; gene.

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Gaps

10;

225

199 284 343

165 139

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protein kinase T518.9 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86431
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chwi, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; W. D.; Yu, G.; Fraser, C.M.; Vohter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; W. D.; Yu, G.; Fraser, C.M.; Vohter, J.C.; Davis, R.W.
A;Hile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Rosldues: 1-53 «MAW»
A;Residues: 1-53 «MAW»
A;Residues: 1-53 «MAW»
C;Cross-references: EMBL:Z21503
C;Genetics:
A;Introns: 54/1; 84/3; 112/3; 144/3; 194/2; 225/3; 294/3; 382/3; 411/2; 448/3; 503/2
C;Superfamily: protein kinase homology
C;Superfamily: protein kinase homology «KIN»
F;69-339/Domain: protein kinase homology «KIN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 LSREGILDALFVLFEECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 NILLDRCGHIRLADFGSCLKIQPDGMVRSLVAVGTPDYLSPEILQAVGGGFGAGSYGFEC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 DWWALGVFAYEMFYGQTPFYADSTAETYAKIVHYREHLSLPLADTVVPEEAQDLIRGLLC 319
                                                                                                                                             A,Cross-references: UNIPROT:P54265; EMBL:221505
R;Mahadevan, M.S.; Amemiya, C.; Jansen, G.; Sabourin, L.; Baird, S.; Neville, Hum. Mol. Genet. 2, 299-304, 1993
A;Title: Structure and genomic sequence of the myotonic dystrophy (DM kinase)
A;Reference number: S38815; MUID:93271990; PMID:8499920
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                                                                                                    A;Residues: 1-557 <MAH>
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A;Status: preliminary
A;Molecule type: DNA
                                                            A; Molecule type: DNA
                    A; Accession: S71829
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                                                                                                                                                                                                                                                                                                                        Scrine/threonine-specific protein kinase (BC 2.7.1.-) isoform II, Rho-associated - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C;Accession: S74245
R;Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A;Title: ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A;Reference number: S74245
A;Title: NOCK-II, two isoforms of Rho-associated coiled-coil forming protein
A;Reference number: S74245
A;Stetus: prataininary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1388 cANK>
A;Cross-references: UNIPROT:P70336; EMBL:U58513; NID:g1514697; PIDN:AAC53133.1; PID:g151
C;Superfamily: protein kinase c zinc-binding repeat homology; protein kinase homology
C;Keywords: phosphotransferase; serine/threonine-specific protein kinase
F;30-354/Domain: protein kinase C zinc-binding repeat homology <KEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-specific protein kinase (EC 2.7.1..) - mouse
NyAlternate names: myotonic dystrophy-associated protein kinase; myotonin protein kinase
C;Species Mus musculus (house mouse)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Aug-2004
C;Accession: S71829; S38815
R;Mahadevan, M.S.; Amemiya, C.; Jansen, G.; Sabourin, L.; Baird, S.; Neville, C.E.; Worm submitted to the EMBL Data library, January 1993
A;Description: Structure and genomic sequence of the myotonic dystrophy kinase (DM kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 853.5; DB 2; Length 1; Pred. No. 5.7e-31; 95; Mismatches 144; Indels
     GILGRSESVVSGLDSPA--KTSSMEKKLLIKSKELQDSQDKCH 466
                                                            444 TSSMEKKLLIKSKELQDSQDKCH 466
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Matches 177; Conservative
                                                                                          LLLS-
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serine/threonine-specific protein kinase (EC 2.7.1.-) orb6 - fission yeast (Schizosacchan
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Accession: T41723
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residus: 1-469 <RIE>
A.Residus: 1-469 <RIE>
A.Cross-references: UNIPROT:013310; EMBL:AL121770; PIDN:CAB57446.1; GSPDB:GN00066; SPDB:&A.Cross-references: UNIPROT:013310; EMBL:AL121770; PIDN:CAB57446.1; GSPDB:GN00066; SPDB:&A.Cross-references: UNIPROT:013310; EMBL:AL121770; PIDN:CAB57446.1; GSPDB:GN00066; SPDB:&A.Cross-references: UNIPROT: P. Commid G821
A.Verde, F.; Wiley, D.J.; Nurse, P.
Proc. Natl. Acad. Sci. U.S.A. 95, 7526-7531, 1998
A.Title: Fission yeast orb6, a ser/thr protein kinase related to mammalian rho kinase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: coordinates maintenance of cell polarity during interphase with the c
A;Note: interacts genetically with orb2, which encodes the Pakl/Shk1 protein kinase
C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase
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                                                                                                                                                                                                                                                                                             442
                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: T43526
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: UAA
A;Residues: 1-469 eVER>
A;Cross-references: EMBL:AP009512; NID:g2443510; PIDN:AAC32420.1; PID:g2443511
C;Genetics:
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                                                                                                                   325
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                                                                                                                                                                                                                                   326 DDPKVSSDFLDLIQSLLCGQKERLKFEG---LCCHPFFSKIDWNNIRNSPPFFVPTLKSD 382
                                                                                                                                                                                                                                                                                                                                                       DDTSNFDEPEKNSWVSSSPCQLSP--SGFSGEELPFVGFSYSKALGILGRSESVVSGLDS 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
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   -- SNKMVNAKLPIGTPDYMA
                                                                                                                                                    329 PEVLL-----KKGYGMECDWWSLGAIMYEMLVGYPPFYSDDPMSTCRKIVNWKNHLKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 PLDCSTLEEKDFSVGDNANGGSRSDSPPAPKRTQQEQLEHWQKNRRMLAYSTVGTPDYIA
                                                                                                                   PEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFP
                                                                                                                                                                                                                                                                                             383 EEAKLSPEAKDIISRLLCNVTERLGSNGADEIKVHSWFKGIDWDRIYQMEAAFIPEVNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 SAKDFEVRSLVGCGHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 DSPWVVSLYYAFQDSLYLYLIMEFLPGGDLMTMLINY-DTFSEDVTRFYMAECVLAIADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th the cell cycle.
A;Reference number: 222544; MUID:98301608; PMID:9636183
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R;Riseger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z22012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 PAKTSSMEKKLLIKS---KELQDSQD 463
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Best Local Similarity 39.21
Matches 148; Conservative
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A,Map position: 1
A;Introns: 48/2; 106/3
C;Function:
245 KMN-
                                                                                                                      566
                                                                                                                                                                                                                                                                                                                                                       383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                            436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAEGTSARTFINIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEG----LCCH 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFDBPEKNSWVSSSPC------QLSPSG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGDLLS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLNRYEDQLDENLIQPYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAA 244
                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein kinase PKTL7 (EC 2.7.1.-) - common tobacco (Species: Nicotiana tabacum (common tobacco) (CjSpecies: Nicotiana tabacum (common tobacco) (CjAccesian: 31-Jan-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004 (CjAccesian: 849077 (KjHuang, Y.) Wan, J.; Ko, K.; Dennis, D.T. (RjHuang, Y.) Wan, J.; Ko, K.; Dennis, D.T. (RjHuang, Y.) Wan, A.; Man, J.; Ko, K.; Dennis, D.T. (RjHuang, Y.) Wan, J.; Ko, K.; Dennis, D.T. (RjHuang, Y.) Wan, J.; Ko, K.; Dennis, D.T. (RjHuang, Y.) Wan, J.; Ko, K.; Man, J.; Ko, K.; Dennis, D.T. (RjHuang, Y.) Wan, J.; Ko, K.; Man, J.; Ko, K.; Man, J.; K.; Man, J.; Ko, K.; Man, J.; Man, J.; Man, J.; M.; Man, J.; M
                                                                                                                                                                                                                                                                                                YMY FERRPDLLTKGTQDKAAAVKLKIENFYQSSVKYAIERNERVELETELTSHNWSEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 LSTGFHKTHDSNYYKKLLQQDEATNGISKPGTYNANTTDTANKRQTMVVDSISLTMSNRQ
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                                                                                                                                              CSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHPAEVQVVREKATGD
                                                                                                                                                                                                                                                               IYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGGD
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Pred. No. 1.4e-24;
74; Mismatches 144; Indels
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Search completed: March 18, 2005, 15:40:47 Job time: 45 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

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US-10-724-594-2 2602 score: Title: Perfect

1 MLKFKYGARNPLDAGAAEPI.........CSRILPSVYAKGSARGRCWL 497 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s: \*
geneseqp2000s: \*
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geneseqp2001s: \*
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geneseqp2003ss: \*
geneseqp2003bs: \* A\_Geneseq\_16Dec04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Abul0126 Novel hum	Aae39504 Human kin	Ado40592 Human kin	Abp97687 Amino aci	Aae16261 Human kin	Abul0127 Variant n	Abp97681 Amino aci	Adn62809 Human NOV	Ada05644 Human NOV	Abb81928 Human kin	Abb81927 Human kin	Aae24150 Human kin	Aao26959 Human CRI	-	Adf60994 Pain asso	Adq89100 Human uro	Human	Adj96610 Human cit	Abg78363 RHO/RAC-i	Ada05642 Human NOV	Adn63228 Human NOV	Adn62807 Human NOV	Abg78362 Human pro	Ada05654 Human NOV	Adn62819 Human NOV
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# ALIGNMENTS

Beasley EM; Human; enzyme; gene therapy; kinase; antisense. Di Francesco V, Ş ABU10126 standard; protein; 497 11-SEP-2002; 2002US-00238709. 13-MAR-2001; 2001US-00804471. entry) (APPL-) APPLERA CORP. (first Webster M, Yan C, Novel human kinase. US2003022340-A1. Homo sapiens. 30-JAN-2003. 11-AUG-2003 ABU10126; RESULT 1 

2003-438978/41. N-PSDB; ACA61394. New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.

Claim 1; Fig 2; 207pp; English.

The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are transgenic animals expressing all or a part of the nucleic acid, for

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monitoring the effectiveness of modulating compounds on the expression cactivity of the transporter gene in clinical trials or in treatment regimen, in gene therapy and as antisenese constructs to control transporter gene expression in cells, tissue and organisms. The present sequence represents the amino acid sequence of a novel human kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; kinase protein; diagnostic; therapeutic; immune response; enzyme;
pharmacogenomic; tissue typing; gene therapy; chromosome 12; transgenic.
                                                                                                                        DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
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93. .96
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ive 0; Mismatches 0;
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New isolated human kinase proteins, useful as models for developing human therapeutic targets, or for treating a disorder associated with an absence of, inappropriate or unwanted expression of the protein, e.g.
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                                                                                     "Protein kinase ATP-binding region signature"
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:e= "Protein kinase C phosphorylation site"
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     drug screening assays, in assays to determine the biological activity of the protein, to raise antibodies and to elicit another immune response. The antibodies are useful in pharmacogenomic analysis, for inhibiting protein function and for tissue typing. The transgenic animals are useful for studying the function of kinase protein, identifying and evaluating modulactors of kinase protein activity. The invention is also used in gene therapy. The present sequence is the human kinase protein. The human kinase gene is located on chromosome 12
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                                                                                                                         Length 497;
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                                                                                                                                             Indels
                                                                                                                       100.0%; Score 2602; DB 7;
100.0%; Pred. No. 2.1e-254;
ive 0; Mismatches 0;
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phosphorylation site"
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/note= "N-78.
                                                                                                                                  Local Similarity 100.
Les 497; Conservative
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                                                                                                    Sequence 497 AA;
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The present invention provides a kinase polypeptide and its encoding polymucleotide. The polypeptide and polymucleotide of the invention are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The invention is also useful for biological assays related to kinases, in drug screening assays, for treating disorders characterized by an absence of inappropriate and
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                                                                                                                                          /note= "Protein kinase ATP-binding region signature"
140. .143
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                       .96
ce= "Casein kinase II phosphorylation site"
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/note= "Protein kinase C phosphorylation
103. .126
"Casein kinase II phosphorylation
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217. .229
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/note= "Pro
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/note= "Pro
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                                                                                                                                                                                                                                                                                                                                 signature"
248. .250
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/note= "N-
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the protein. The present sequence is the human
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                                               Length 497;
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Pred. No. 2.1e-254;
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expression
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                            Sequence 497 AA;
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          kinase protein.
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10-DEC-2001;
25-APR-2002;
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                                                                                                                                                                                                                                                                                 The present sequence represents a human citron rho/rac-interacting kinase-short kinase polypeptide. The polynucleotide and polypeptide of the invention are useful in preventing, ameliorating, or treating diseases associated with the polypeptide dysfunction. The expression vector or the reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase-short kinase in a disease, such as obesity or chronic obstructive pulmonary disease. These may also be used for treating obesity/ overweight-associated comorbidities, such as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced fertility, and depression
                                                                                                                                                                                                                                                                                       kinase
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                                                                              New human citron rho/rac-interacting kinase-short kinase polypeptide and polynucleotide for preventing or treating diseases associated with the polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary
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Matches 496; Conservative
WPI; 2003-221595/21
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                              N-PSDB: ABZ68726
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Human; kinase; PXIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis; maune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AlDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; haparitis; hypothyroidism; cerebral palsy; cararact; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy.
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Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
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/note= "Protein kinase C terminal domain"
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/note= "Bukaryotic protein kinase
98. .241
/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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/label= Protein_kinase_domain
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AAE16261 standard; protein; 497
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23-JUN-2000; 2000US-0213467P.
30-JUN-2000; 2000US-0215651P.
07-JUL-2000; 2000US-0216652P.
13-JUL-2000; 2000US-0228056P.
25-AUG-2000; 2000US-0228056P.
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                                                                                                                                                                    Human kinase PKIN-7 protein
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The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition associated with decreased expression of treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The clisociate include cancer (leuksemia, adenocarcinoma, lymphoma, melanoma, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, disbetes autoimmune thyroiditis, gout, bronchitis, Crohn's disease, disbetes mellitus, multiple sclerosis, Good pasture is syndrome, gravelitis, ulcerative colitis, relevanted arthritis, slogren 's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, aneurysms, congestive heart failure, angina pectoris, myocarditis, aneurysms, congestive heart failure, angina pectoris, myocarditis, consense (atteriovenous fiscula, hypertension, vasculatis, lipid disorder (fatty liver, Fabry's disease, ulceman-Pick's disease, chronic bronchitis, lumours); lipid disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, chronic bronchitis, lumours); lipid clisocher test compound and in gene therapy. The present sequence is human provented to the presented to the presen
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  cancer, comprise human kinase polypeptides.
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                                                   Claim 1; Page 146-147; 197pp;
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RESULT 6 ABU10127

New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as

WPI; 2002-090207/12 N-PSDB; AAD26454.

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The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for monitoring the effectiveness of modulating compounds on the expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence is not shown in the specification but indexer using the information given in figure 3
                                                                                                                                                                                                                                                                      /note= "Wild-type Trp substituted by Cys as a result of single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity of the transporter gene in clinical trials or in treatment regimen, in gene therapy and as antisense constructs to control transporter gene expression in cells, tissue and organisms. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents the amino acid sequence of a variant novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beasley EM;
                                                                                                                                                    Human; enzyme; gene therapy; kinase; antisense.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yan C, Di Francesco V,
                                                                                                                                                                                                                                 Location/Qualifiers
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ABU10127 standard; protein; 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2001; 2001US-00804471
                                                                                                                 Variant novel human kinase.
                                                                               entry)
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                                                                                                                                                                                             Homo sapiens
                                                                         11-AUG-2003
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                                      ABU10127
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ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
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                                                                          1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
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Length 497;
                            1; Indels
99.5%; Score 2589; DB 6; 99.8%; Pred. No. 4.5e-253;
                            0; Mismatches
                           496; Conservative
               Local Similarity
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Query Match
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Matches
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ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHPAEVQVVREKATG 120

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121 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human citron rho/rac-interacting kinase-short kinase polypeptide ar polynucleotide for preventing or treating diseases associated with the polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human citron rho/rac-interacting kina-short kinase polypeptide. The polynucleotide and polypeptide of the invention are useful in preventing, ameliorating, or treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chronic obstructive pulmonary disease; hypertension; diabetes; coronary artery disease; hyperlipidaemia; stroke; gallbladder disease; gout; osteoarthritis; sleep apnea; cancer; thrombolic disease; polycystic ovarian syndrome; fertility; depression.
361 SKIDCNNIRNSPPFFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS
                                                                                                                                                                                                                                                                                                   421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVPISAAGLLPCSR
                                           DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                                                             DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                                                                                                     GSAAKMISIKKMINAKLPIGTPDYMAPEVLTVMIGDGKGTYGLDCDWWSVGVIAYEMIYGR
                                                                                                                      241 GSAAKANSNKAVNAKLPIGTFDYMAPEVLTVANGDGKGTYGLDCDWASVGVIAYEMIYGR
                                                                                                                                                              SPFAEGTSARTFUNIMNFORFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF
                                                                                                                                                                                       301 SPFAEGTSARTFNNIMNFORFLKFPDDPKVSSDFLDLIQSLLCGOKERLKFEGLCCHPFF
                                                                                                                                                                                                                       SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGEELPFVGFS
                                                                                                                                                                                                                                                                                  YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of citron rho/rac-interacting kinase-short kinase.
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2002US-0375015P.
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                                                                                                                                                                                                                                                                                                                                                            481 ILPSVYAKGSARGRCWL
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10-DEC-2001; 2
25-APR-2002; 2
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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 100-101; 586pp; English

The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
CC diseatifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
cuse in treating a pathology that is related to an aberrant expression or
aborrant physiological interactions of the polypeptide, (11) a method of
cc above; (10) a method for identifying of the polypeptide; (11) a method of
cc apathology associated with the polypeptide; (11) a method of
cc are publication of activity or of latency or predisposition to
cc a pathology associated with the above polypeptide. NOVX
cs preventing a pathology passociated with the above polypeptide in a
cc mammal; and (14) a method for producing the above polypeptide. NOVX
cs gequences have antidabetic, anorectic, antibacterial, virucide,
confinityaemic activities, and can be used in gene therapy. The
colypeptide is useful in manufacturing a medicament for treating a
colypeptide is useful in manufacturing a medicament for treating colypeptide associated with a human disease. The polypeptide or the mucleic
cacid molecule may be disease uch as Alzheimer's disease or perkinson's
cc disease, immune disorders such as Alzheimer's disease or perkinson's
cc disease, immune disorders such as Alzheimer's and each or perventive medicine and
cp pragentice in particulation.
CC dyslipidaemias. The nucleic aci

Sequence 623 AA;

240 GSAAKMISIKWYVIAKLPIGTPDYMAPBVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180 DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 184 SPFAEGTSARTFANIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 364 9 64 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQCKPPFWTQQQMSPLSREGILDALFVLFB 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF GSAAKMISNKAVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF Gaps ö Length 623; 0; Indels Score 2440; DB 6; Pred. No. 8.6e-238; 2; Mismatches 0; 93.8%; Matches 466; Conservative Best Local Similarity 245 'n 61 9 121 125 181 185 241 301 Query Match 셤 ઠે g ò 요 ò 요 ઠે g 8

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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly ditron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in disagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, 424 120 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHPAEVQVVREKATG 120 121 DIYAMKVMKKKALLAQEQVSFFBEBRNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180 361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420 9 9 in gene kinase; enzyme; serine-threonine kinase; nootropic; cytostatic; rho-interacting kinase; gene therapy; mental disorder; cancer. 365 SKIDWANIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG Gaps Novel polynucleotide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, it therapy of disorders and diseases e.g. cancer and pharmacogenomic applications. biological or medical disorders and diseases including cancer. The sequence represents a novel human kinase of the invention .; 0 425 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 472 Length 1958; 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV Indele ö Score 2440; DB 5; Pred. No. 5.7e-237; 2; Mismatches Claim 4; Page 46-50; 50pp; English. ABB81928 standard; protein; 1958 Miranda M, Friddle CJ 20-DEC-2001; 2001WO-US050497. (LEXI-) LEXICON GENETICS INC. 27-DEC-2000; 2000US-0258335P. 93.8%; 99.6%; (first entry) Matches 466; Conservative 2002-599796/64. Best Local Similarity Sequence 1958 AA; N-PSDB; ABQ78871 WO200259325-A2 Homo sapiens. Human kinase 10-OCT-2002 01-AUG-2002. ABB81928; Query Match Human; RESULT 10 **ABB8192** 셤 셤 셤 ò ઠે

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DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG 180
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                                                                              GSAAKMISIKAVNAKLPIGTPDIMAPEVLTVANGDGKGTYGLDCDWWSVGVIAYEMIYGR
                                  SPFAEGTSARTFINIMNFORFLKFPDDPKVSSDFLDLIQSLLCGOKERLKFEGLCCHPFF
                                                                                                                      SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDL1QSLLCGQXERLKFEGLCCHPFF
                                                                                                                                                                                                                                                                                                                                                                  cytostatic;
                    DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
                                                                GSAAKWNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR
                                                                                                                                                     SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGEELPFVGFS
                                                                                                                                                                           SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS
                                                                                                                                                                                                                                                                                                                                                                 serine-threonine kinase; nootropic; cytostatic;
kinase; gene therapy; mental disorder; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, in therapy of disorders and diseases e.g. cancer and pharmacogenomic
                                                                                                                                                                                                             YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468
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                                                                                                                                                                                                                                                                             standard; protein; 2054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LEXI-) LEXICON GENETICS INC.
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                                                                                                                                                                                                                                                                                                                        entry
                                                                                                                                                                                                                                                                                                                                                                 Human, kinase; enzyme;
Citron rho-interacting
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                                                                                                                                                                                                                                                                                                                                           Human kinase
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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly citron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence represents a novel human kinase of the invention

Sequence 2054 AA;

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                                                                                                                                                                                                                                                      DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG
                                                                                                              1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE
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                                                                                                                                                                                                                       ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
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  Length 2054;
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Score 2440; DB 5;
Pred. No. 6.1e-237;
2; Mismatches 0;
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'note= "Protein kinase domain"
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Query Match 93.8%;
Best Local Similarity 99.6%;
Matches 466; Conservative
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SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
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RASTELLI L.
STONE D J.
SHENY C B A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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CATTERTON E.
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PEYMAN J I
KEKUDA R.
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 reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase-short kinase in a disease, such as obesity or chronic obstructive pulmonary disease. These may also be used for treating obesity/ overweight-associated comorbidities, such as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, ostecarthritis, sleep apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced fertility, and depression
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 the polypeptide dysfunction. The expression vector or the
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                                                                                                                                          Query Match 99.2%; Score 2582; DB 6; Best Local Similarity 99.8%; Pred. No. 2.3e-252; Matches 494; Conservative 1; Mismatches 0;
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associated with
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421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKV

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The invention relates to isolated NoVX polypeptides and polymucleotides.

NoVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abberrant expression and activity of NoVX polypeptides.

Co treat a medical condition in human related to the abberrant expression and activity of NoVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists and antagonists and antagonists and antagonists and activity of NOVX. Co lead to modulate NOVX polymucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies, agonists may also be used as diagnose and treat: metabolic disorders, diabetes, obesity, infectious diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, alzheimer's Disease, parkinson's bisorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic disturbances associated with chronic diseases and various cancers.

They may also be used as antibacterial agents. The present sequence of a human NOVX protein.
     Berghs C, Dipippo VA;
                                                                                                                                                            Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
  g ME, Leach MD, Agee ML
Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4; 395pp; English
  RA, Rothenberg ME,
Gangolli EA, Rieg
                                                                            WPI; 2004-213931/20.
N-PSDB; ADN62808.
Shimkets RA,
                              Eisen A,
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Sequence 620 AA;

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240
                                                                                                                                   ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120
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                                                                    1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLFE
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                                   0; Gaps
93.8%; Score 2440; DB 8; Length 620; 99.6%; Pred. No. 8.5e-238; Live 2; Mismatches 0; Indels
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Matches 466; Conservative
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Dipippo VA;
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                                                                                                                                                                          human, NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; metrabolic disorder; Alzheimer's disease; Parkinson's disease; immune disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
             425 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 472
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OY 361 SKIDWANIENSPPPVPTLKSDDDTSNPDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420	OY 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480	Oy 481 ILPSVYAKGSARGKCWL 497 	121 02	; Sequence 2, Application 05/10/24954; Publication No. US20040091993A1; GENERAL INFORMATION: APPLICANT; WESSTER, MARION 41.	; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES ; TITLE OF INVENTION: THEREOF ; FILE REFERENCE: CLOOI164DIV II ; CURRENT APPLICATION NUMBER: US,10/724,594	CURRENT FILING DATE: 2003-12-02  NUMBER OF SEQ ID NOS: 4  SOFTWARE: PastSEQ for Windows Version 4.0  SEQ ID NO 2  IENOTH: 497  TYPE: PRT  ORGANISM: Homo sapiens	Query Match 100.0%; Score 2602; DB 15; Length 497; Best Local Similarity 100.0%; Pred. No. 4.9e-190; Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 MLKFKYGARNPLDAGAAEPIANRASRLNLFFQGKPPFWTQQQMSPLSREGILDALFVLPE 60	Qy 61 ECSQPALMKIKHVSNPVRKYSDTIAELQPELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120	OY 121 DIXAMKVMKKKALLAQEQVSFFEEENILSRSTSFWIPQLOYAFQDRNHLYLVWEYQPGG 180	QY 181 DLLSLINRYEDQLDENLIQEYLAELILAVHSVHLMGYVHRDIKFENILVDRTGHIKLVDF 240	OY 241 GSAAKONISNIKOVINAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYER 300  241 GSAAKONISNIKOVINAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR 300	Qy 301 SPFABGTSARTENNIMNFORFLKFPDDPKVSSDFLDLIQSLLCGGKERLKFBGLCCHPFF 360 301 SPFABGTSARTENNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGGKERLKFFGLCCHPFF 360	Qy 361 SKIDWNNIRNSPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420	Qy         421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLJIKSKELQDSQDKCHKVPISAAGLLPCSR 480           Db         421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLJIKSKELQDSQDKCHKVPISAAGLLPCSR 480	Oy 481 ILPSVYAKGSARGRCWL 497 
QY 181 DLESLINRYEDQLDENLIQPYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240	QY 241 GSAAKANSNKAYNAKLPIGTPDYMAPEVLTVANGDGKGTYGLDCDKWSVGVIAYEMIYGR 300	QY 301 SPFABGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360	QY 361 SKIDWANIENSPPEVPTLKSDDDTSNFDEBEKNSWVSSSPCQLSPSGFSGELFFVGFS 420	Qy 421 YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKVFISAAGLLPCSR 480	Qy       481 ILPSVYAKGSARGRCWL 497         Db       481 ILPSVYAKGSARGRCWL 497	Si Si Ti	; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES ; TITLE OF INVENTION: THEREOF ; FILE REFERENCE: CLOO1164DIV ; CURRENT APPLICATION NUMBER: US/10/238,709	0,	ģ	Query Match Best Local Similarity 100.0%; Score 2602; DB 14; Length 497; Best Local Similarity 100.0%; Pred. No. 4.9e-190; Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 MLKFKYGARNPLDAGAAEPIANRASRLNIFFQGKPFFMTQQQMSPLSREGILDALFVLFE 60	Qy 61 ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG 120	QY 121 DIYAMKWAKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDRNHLYLVMEYQPGG 180 Db 121 DIYAMKWAKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDRNHLYLVMEYQPGG 180	QY 181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240 Db 181 DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF 240	Qy 241 GSAAKANSNKAVNAKLPIGTPDYMAPEVL/TVANGDGKGTYGLDCDWWSVGVIAYEMIYGR 300	Qy 301 SPFAEGTSARTFNNIMNPQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF 360 

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 18, 2005, 15:40:07; Search time 146 Seconds

Run on:

(without alignments) 1125.198 Million cell updates/sec

Perfect score:

US-10-724-594-2 2602 1 MLKFKYGARNPLDAGAAEPI......CSRILPSVYAKGSARGRCWL 497

Sequence:

Scoring table:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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100.0		497	14	US-10-238-709-2	Sequence 2, Appli
100.0		497	15	US-10-724-594-2	Sequence 2, Appli
99.5		497	15	US-10-311-034-7	Sequence 7, Appli
93.8		623	15	US-10-262-511-4	Sequence 4, Appli
93.8		1958	13	US-10-028-946-4	Sequence 4, Appli
93.8		2054	13	US-10-028-946-2	Sequence 2, Appli
93.8		2054	15	US-10-415-011-21	Sequence 21, Appl
93.4		2053	13	US-10-017-216-2	Sequence 2, Appli
93.4		2053	14	US-10-325-430-12	Sequence 12, Appl
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92.9		2055	16	US-10-618-941-67	Sequence 67, Appl
92.7		2053	11	US-09-964-956-11	Sequence 11, Appl

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4 11 11 11 11 12 12 12 12 12 12 12 12 12

# ALIGNMENTS

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TITLE OF INVENTION: ISOLATED HUGAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ISOLATED HUGAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREW BALLAND NUMBER: US/09/804,471A CURRENT APPLICATION NUMBER: 201-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
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                  Sequence 2, Application US/09804471A Patent No. US20020132322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
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catherosclerosis, multiple sclerosis, psoriasis), disorders affecting growth and development (e.g., arreriosclerosis, cirrhosis, hepatitis), cardiovascular disorder (e.g., hypertension, myocardial infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver, Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia, hypertipidaemia, obesity), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a disquostic test for a condition or a disease associated with the expression of PKIN in a condition or a disease associated with the expression of FKIN in a antegonist of PKIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN. CHIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, and in somatic or germline gene therapy. The present sequence is human

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Lal PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders.
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NJA, Nguyen DB;
Tribouley CM, La
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Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen
R, Lu Y Xue H, Burford N, Bandman O, Tribouley (
SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A),
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                                                                                                                                                                                                                                                                                                                                                                                                 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG
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                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                 Score 2440; DB 5; Length 2054;
Pred. No. 6.1e-237;
2; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                   Query Match 93.8%;
Best Local Similarity 99.6%;
Matches 466; Conservative
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                                                                                                                                                                                                                                                                       Sequence 2054 AA;
                                                                                                                                                                                                                                      PKIN protein
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The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing, treating and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,

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361 SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGFS 420
                                                   241 GSAAKANSNKAVNAKLPIGTPDYMAPEVLTVANGDGKGTYGLDCDWWSVGVIAYEMIYGR
                                                                                                                                          301 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF
                                                                                                                 SPFAEGTSARTFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein; tumourigenesis; tumour growth; tumour metastrasis; viral infection; skeletal muscle disorder; muscular dystrophy; myotonic dystrophy; immune disorder; neoplastic disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Serine/Threonine protein kinase active site
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                                                                                                                                                                                                                                                                                                                                   YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKM 468
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1568. .1865
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/note= "CNH domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human citron rho/rac-interacting kinase (CRIK) polypeptide polynucleotide, useful in preventing, ameliorating or treating associated with human CRIK dysfunction, e.g. obesity, diabetes
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Pred. No. 6.1e-237;
2; Mismatches 0;
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                                                                                                                                                                                                                                02-JUL-2001; 2001US-0301841P.
11-DEC-2001; 2001US-0338651P.
25-APR-2002; 2002US-0375014P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease.
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les 466; Conserv
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                                                                                           WO2003004523-A1
diabetes; pain.
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(MDPK) polypeptides designated as 13245 and nucleic acid molecules encoding such polypeptides. 13245 molecules are used to develop diagnostic and therapeutic agents for prognosticating, diagnosting, preventing, inhibiting, alleviating or curing MDPK-related diagnostic. Polypeptides of the invention are used to develop diagnostic and therapeutic agents for 13245-mediated or related disorders such as tumourigenesis, tumour agrowth, tumour metastasis, viral infection of a cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies), immune disorders and neoplastic disorders. The invention is also used in gene therapy. The present sequence is human MDPK protein
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99.1%; Pred. No. 6.3e-236;
iive 3; Mismatches 1;
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Matches 464; Conservative
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The present invention relates to a method for identifying a compound capable of modulating pain or painful disorders. The method comprises assaying the ability of the compound to modulate specific nucleic acid expression or polypeptide activity e.g. potassium channel, or kinase expression/activity. The method and compounds are useful for treating pain or painful disorders e.g. inflammatory pain, chronic pain, neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache pain and tissue pain. The present sequence represents a human protein associated with pain.
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Pred. No. 6.3e-236;
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SUMMARIES	ID	PCT-US03-11189-1	US-10-450-763-15557	US-10-450-763-29273	US-10-450-763-21232	US-10-450-763-13871	PCT-US03-11189-11	PCT-US04-42360-13	PCT-US03-11189-7	US-10-450-763-17152	US-11-060-756-1334	US-11-060-756-1335	US-11-060-756-5606	US-11-060-756-5607	PCT-US03-11189-9	PCT-US03-11189-6	PCT-US04-42360-673	US-10-932-182A-2150	PCT-US03-11189-8	US-10-932-182A-2703	US-10-932-182A-79012	US-10-932-182A-81056	PCT-US03-11189-10	PCT-US03-35712-114	PCT-US03-35712-115
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US-10-287-436A-132 US-10-287-436A-748 US-10-932-182A-2262 US-10-932-182A-2262 US-10-932-182A-2262 US-11-059-535-455 PCT USO4-42360-1108 US-11-059-535-2455 PCT USO3-35712-111 US-11-063-691-1 US-11-063-691-1 US-11-060-756-8116 US-11-060-756-8116 US-11-060-756-8116 US-11-060-756-8116 US-11-050-311189-59 PCT-USO3-11189-59 PCT-USO3-11189-59 US-60-655-875-93506 US-60-655-875-93506 US-60-655-875-93506	ALIGNMENTS	ULT 1  -USO3-11189-1  equence 1, Application PC/TUSO311189  equence 1, Application PC/TUSO311189  ENERAL INPORMATION:  TILLE OF INVENTION: WOVEL POLYNUCLECTIDES ENCODING  TILLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021  FILE REFERENCE: D0193 PCT  CURRENT FILING DATE: 2003-04-11  PRIOR APPLICATION NUMBER: U.S. 60/372,745  PRIOR PELING DATE: 2002-04-12  NUMBER OF SEQ ID NOS: 77  EQ ID NO 1  LENGTH: 957  TYPE: DNA  ORCANISM: Homo sapiens  NAME/KEY: CDS  LOCATION: (1)(957)  -USO3-11189-1	Score 945.4; DB 1; Pred. No. 1.5e-240; 0; Mismatches 1;	TCAAATATGGGGGGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG 	CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 	CTCCTCTTTCCCGAGAAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAGAAAATGCAGTC 	agcctgctctgatgaagattaagcacgtgagcaactttgtccggaagtattccgacacca 
6.2 2945 6 6.2 2945 6 6.2 17224 6 6.1 2137 1 6.1 2137 1 6.1 2137 1 7.1 2137 1 7.2 6 7 7 8 7.3 1400 8 7.4 1400 8 7.6 2577 9 7.6 6 7 7 8 7.7 1400 8 7.6 2577 9 7.7 1400 8 7.7 1400		SULT 1 Sequence 1, Application PC/TUS0311189 GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: POLYBEPTIDE, BMSNKCLITLE OF INVENTION: POLYBEPTIDE, BMSNKCLICHERNY APPLICATION: POLYBEPTIDE, BMSNKCLICHERNY APPLICATION NUMBER: U.S. 60/372,745 PRIOR FILING DATE: 2003-04-11 PRIOR APPLICATION NUMBER: U.S. 60/372,745 PRIOR FILING DATE: 2002-04-12 SPIOR FILING DATE: 2002-04-12 SPIOR FILING DATE: 2002-04-12 SOFTWARE: PATENTING DATE: 2002-04-12 SOFTWARE: PATENTING DATE: 2002-04-12 SEQ ID NO 1 LENGTH: 957 TYPE: DNA ORGANISM: HOMO SADIENS FRATURE: NAME/KEX: LOCATION: (1)(957)	63.8% milarity 99.9% Conservative	rcaaatatggagcgcgg 	CCTCCAGGCTGAATCTG1 	TCCTCTTTCCCGAGAAC	AGCCTGCTCTGATGAAGA 
25 26 27 27 28 29 30 31 31 31 31 31 32 33 34 34 35 36 37 37 38 38 38 38 38 38 38 38 38 38		RESULT 1 PCT-US03-11189-1 Sequence 1, Applic, SERREAL INFORMATIO APPLICANT: BILIGO, ITILE OF INVENTIO) FILE REFERENCE: DO CURRENT APPLICATI CURRENT APPLICATI CURRENT APPLICATI CURRENT APPLICATION PRIOR APPLICATION PRIOR PILING DATE CURRENT APPLICATION PRIOR FILING BATE CURRENT APPLICATION SOFTWARE: PATURE: NAME/KEY: CDS LOCATION: (1)(1) PCT-US03-11189-1	Query Match Best Local Si Matches 946;	Oy 1 T	Oy 61 C	Oy 121 C Db 131 C	Qy 181 A       Db 191 A
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   Length 1048;
                                   Indels
Score 925; DB 7; I
Pred. No. 3.7e-235;
0; Mismatches 5;
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8.210-450-763-29273
; Sequence 29273, Application US/10450763
; GENERAL INFORMATION:
Query Match
Best Local Similarity 99.5%;
Matches 928; Conservative
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LOCATION: (412)...(909)
COTHER INFORMATION: 77% homologous to Mus musculus Pro-Pol-dUTPase
COTHER INFORMATION: polyprotein, accession number Y12713, Smith-Waterman Score=685.
US-10-450-763-15557
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                                                                                         CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG
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                                                                     CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL.
FILE REBERBER: 790CTP9/US
CURRENT APPLICATION WIMBER: US/10/450, 763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/549,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 15557
LENGTHAN 1048
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US-10-450-763-15557
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NAME/KEY: SIMILAR
LOCATION: (3137)...(5767)
OTHER INFORMATION: 79% homologous to Homo sapiens Human myotonic dystrophy gene
OTHER INFORMATION: protein, accession number R41001, Smith-Waterman Score=3811.
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CLUSTOM
SEQ ID NO 21232
LENGTH: 6303
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GENERAL INFORMATION:
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US-10-450-763-21232
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OTHER INFORMATION: 31% homologous to Homo sapiens Human myotonic dystrophy
OTHER INFORMATION: protein, accession number R41001, Smith-Waterman Score=777.
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HAPLICANT: Hyeeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
FRIOR APLICATION NUMBER: PCT/US01/08631
FRIOR PILING DATE: 2001-03-30
FRIOR PILING DATE: 2000-03-31
FRIOR PILING DATE: 2000-03-31
FRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CLSCOME
SOF
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Pred. No. 5.9e-50;
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Best Local Similarity 54.0%;
Matches 534; Conservative
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ORGANISM: Homo sapiens
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SEQUENCE 13811, Application US/10450763
GENERAL INFORMATION:
APPLICANT: Hyeeq, inc.
TILLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL;
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 13871
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LENGTH: 5754 TYPE: DNA ORGANISM: Homo sapiens

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LOCATION: (1)...(411)
COTHER INFORMATION: 95% homologous to Escherichia coli RF-3/Tos, accession number
CHER INFORMATION: D17724, Smith-Waterman Score=665.
US-10-450-763-13871
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Pred. No. 1.6e-46;
0; Mismatches 553;
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Best Local Similarity 50.9%;
Matches 590; Conservative
SIMILAR
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                                                                                                                                                                                                                                                  Score 196; DB 1; Length 53
Pred. No. 5.5e-42;
0; Mismatches 570; Indele
                                                                                                ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Refeeq / NM_053620
DATABASE ENTRY DATE: 2003-10-05
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 49.5%;
Matches 573; Conservative
     script
SOFTWARE: Perl
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                          SEQ ID NO 13
LENGTH: 5333
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GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts General
CGGCTGGGGCAGAATGGAATAGAGGATTTCAAAAAGCATGCGTTTTTTGAAGGTCTAAAT 1038
                                                                                             TGGGAAAATATACGAAACCTAGAAGCACCTTATATTCCTGATGTGAGCAGTCCCTCTGAC 1098
                                                                                                                                                 ACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCTCGTGCCAGCTG 1202
                                                                                                                                                                                                ACATCCAACTICCACGTGGATGACGACGTGCTGGAAAACACGGAAATATTACCTCCTGGT 1158
                                                                                                                                                                                                                                                                                                 1159 rcrcacacacáciriricrecarracarriccarricarrecririracarricacaacecaa 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
FILE REPERRNCE: D0193 PCT
CURRENT APPLICATION NUMBER: PCT/US03/11189
CURRENT FILING DATE: 2003-04-11
PRIOR PILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 11
LENGTH: 204
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                                                 TGGAACAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCTTCAAGTCCGACGATGAC
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TITLE OF INVENTION: Nuclectide sequences involved in pain
FILE REFERENCE: 17633/2048
CURRENT APPLICATION NUMBER: PCT/USO4/42360
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION UNDER: 60/531,341
PRIOR PILING DATE: 19-Dec-2003
NUMBER OF SEQ ID NOS: 2587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 202.4; DB 1;
Pred. No. 4.5e-44;
0; Mismatches 1;
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Best Local Similarity 99.5%;
Matches 203; Conservative (
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ORGANISM: Homo sapiens
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PCT-US03-11189-11
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CAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTAAAATTGAC 1082
                                                                                                                                                                                        1143 ACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCCTCCGTGCCAGCTG 1202
                                                                                                                                                                                                                                      1147 ACGTCCAACTTCGATGACGATGACGTGCTGAGAAACATCGAAATCTTACCTCCCGGC 1206
                                                                                                                                                                                                                                                                                      1203 AGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACAGCAAGGCA 1262
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GENERAL INFORMATION:
APPLICANT:
Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL POLYPEPTIDE, BMSNKC_0020/0021
FILE REPERENCE: D0193 PCT
FILE REPERENCE: D0193 PCT
CURRENT APPLICATION NUMBER: PCT/US03/11189
CURRENT FILING DATE: 2003-04-11
PRIOR PLICATION NUMBER: U.S. 60/372,745
PRIOR PLICATION NOVEL: 2002-04-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIB3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
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Matches 176; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Would:
Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
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Pred. No. 1.3e-36;
0; Mismatches 229;
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; OTHER INFORMATION: n = a,t,c
US-10-450-763-17152
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Best Local Similarity 58.4%;
Matches 326; Conservative
PRIOR FILING DATE: 2000-08-2
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 17152
LENGTH: 4055
                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: Wyeth
APPLICANT: Woth
APPLICANT: Woth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: 18/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 5607
LENGTH: 489
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
TITLE OF INVENTION: POLYPEPTIDE, BMSNKC_0020/0021
FILE REFERENCE: DOLYDEPTIDE, BMSNKC_1020/0021
CURRENT APPLICATION NUMBER: PCT/US03/11189
CURRENT FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: U.S. 60/372,745
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Pred. No. 7.2e-36;
A. Mismatches 2;
                                                                                                                                                                                                                          Score 171.8; DB 8;
Pred. No. 7.2e-36;
0; Mismatches 2;
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GENERAL INFORMATION:
                           NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 5606
LENGTH: 489
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98.9%;
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98.9%;
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Best Local Similarity 98.9
Matches 173; Conservative
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Best Local Similarity 98.9
Matches 173; Conservative
                                                                                                                            TYPE: DNA
GRGANISM: Homo sapiens
US-11-060-756-5606
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CORGANISM: Homo sapiens
US-11-060-756-5607
       CURRENT FILING DATE:
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Taraget Genes
FILE REPERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PATENTIN version 3.2
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Woth
TITLE OF INVENTION: Target Genea
TITLE OF INVENTION: Target Genea
FILE REFERENCE: AM101083 (03185-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
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                                                                                                                                                                                                                                            Score 171.8; DB 8; Length 489;
Pred. No. 7.2e-36;
0; Mismatches 2; Indels 0
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENY FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1335, Application US/11060756
GENERAL INFORMATION:
APPLICANT: Wyeth
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.9%;
Matches 173; Conservative
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Best Local Similarity 98.9
Matches 173; Conservative
                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-11-060-756-1334
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US-11-060-756-1335
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                                                                                             SEQ ID NO 1334
LENGTH: 489
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507 GICATGGAATATCAGCCTGGAGGGACTTGCTGTCACTTTTGAATAGATATAGAGGACCAG 566
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; Sequence 6, Application PC/TUS0311189
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVEXNION: NOVEL POLYNUCLESOTIBES ENCODING THE HUMAN CITRON KINASE
; TITLE OF INVEXNION: POLYPEPTIDE, BMSNKC_0020/0021
; FILE REPERENCE: D0193 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/11189
; CURRENT PILING DATE: 2002-04-12
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 142
                                                                                                                                                                                                                                                                                                                                                               87 GGGAAACCACCTTTATGACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTA 146
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PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.2
SEQ ID NO 9
LENGTH: 143
                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
PCT-US03-11189-9
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ORGANISM: Homo sapiens
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pna/US107B_COMB.seq:*
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pna/US108B_COMB.seq:*
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7: /cgn2_6/ptodata/1/pna/USO9_COMB.seq:*
7: /cg
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	equence 1	ייי פייי	ednence 9	'n	e O	m	'n	1, 7	43,	1679	Sequence 3, App	11,	Sequence	equence 10,	51,	equence 1, A	e 10,	51, 7	Sequence 41,	1, Api	Sequence 1,	ď	O)	e 1,	ų	13,	e 8,	e 13,	e 13,	1047	Sequence 10	416	419	e 416	H	equence 1555	quence 1	٠.	g	Sequence 10200, A	Sequence 30150, A	9	e 158	Sequence 15814, A	equence 45
3 ID	62 US-10-724-594-1	2 US-10-311-034-	0 US-60-215-65	-US02-31373-	1 US-10-262-511-	-262-511A	2 US-10-791-666-	US-10-791	US-10-415-011	-235	6 US-10-017-216-3	PCT-US02-41011	2 US-10-325-430-1	PCT-US02-41011-	PCT-US04-00750-5	6 US-10-017-216-1	2 US-10-325-430-1	2 US-10-757-262	15 US-60-457-901	PCT-US03-21730-	8 US-10-618-941-	31373-	-964-956	1 US-10-262-511-	1 US-10-262-511A	02-31373-1	US-09-964-956	1 US-10-262-511-13	1 US-10-262-5	8 US-10-144-771-1047	06 US-60-360-207-1	PCT-US02-01222-4	8 US-10-120-988-41	5 US-10-470-868-41	4 US-10-412-897-1	-08631-	PCT-US02-23268-1	5 US-10-932-349	20 US-60-500-33	-09-699-998-1	34 US-09-785-276A-30150	-10-357-930-3	34 US-09-785-276A-15814	53 US-10-357-930-15814	34 US-09-785-276A-45643
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Score	1481	6	76.	388.	1388.2	1388.2	388.		1388.2	1388.2	•	1381.8		1381.8	•	1381.8		1381.8	1381.8	1372	13	'n	65.	365.	365.	365.	365.	365.	365.	110.		47.	47.	47.	945.4		44	45	645.8	578.8	578.8	578.8	441.8	441.8	m
Result No.	-	0	m	4	S	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32				36				40	4	c 42	4	4	4

ALIGNMENTS

RESULT 1  US-10-724-594-1  Sequence 1. Application US/10724594  GENERAL INFORMATION:  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  TITLE OF INVENTION: THEREOF  TITLE OF INVENTION: THEREOF  TITLE OF INVENTION: 2003-12-02  CURRENT APPLICATION NUMBER: US/10/724,594  CURRENT FILING DATE: 2003-12-02  NUMBER OF SEQ ID NOS: 4  SOFTWARE: FRASEQ for Windows Version 4.0  LENGTH: 1515  TYPE: DNA  CURRENT: DNA  SEQ ID NO 1  LENGTH: 1515  TYPE: DNA  CORGANISM: Homo sapiens	y Match 100.0%; Score 1481; DB 62; Length 1515; Local Similarity 100.0%; Pred. No. 0;	1 TCAAATATGGAGGGGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGG 60	61 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120 	121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAGAAGGAGTC 180	181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA 240	241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG 300	301 GITGIGGICACITIGCIGAAGIGCAGGIGGIAAGAGAAAGCAACCGGGGACAICTAIG 360 	361 CTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 420 	421 AAGAGGGAACATATTATCTGGAAGCACAAGCCGTGGATCCCCCAATTACAGTATGCCT 480	481 ITCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540 	541 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600 	601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660	661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGATTTTGGATCTGCCG 720 	721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780
RESULT 1 US-10-724-1 SEQUENCE GENERAL TITLE OI SOUTHERT SOUTHERT TITLE OI T	Query M Best Lo Matches	& <del>8</del>	SP SS	çy qa	y da	oy da	ζς Q	ço qa	දු දු	දු දු	상 음	장 음	S S	ò

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CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3951059CB1
US-10-311-034-33
                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                           APPLICANT: DING, Li
APPLICANT: GRETHER, Megan
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, CRaig H.
ITLE OF INVENTION: HUMAN KINASES
                                                                      HAFALIA, April
ARVIZU, Chandra S.
GURURAJAN, Rajagopal
IO, Terence P.
                                                                                                                                                                                              POLICKY, Jennifer L
                                                                                                                                         KHAH, Farrah A.
RECIPON, Shirley A.
AZIMZAI, Yalda
                                      HE, Ann
THORNTON, Michael
                     BAUGHN, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
     TANG, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 33
LENGTH: 2066
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                                                                                                                                                                                            CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960
737 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 796
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GANDHI, Ameena R.
TRIBOLLEY, Catherine M.
CHAWLA, Narinder K.
YAO, Wonique G.
LU, Dyung Aina M.
GREENWALD, Sara R.
RAMKUWAR, Jayalaxmi
GRIFFIN Jennifer A.
KEARNEY, Liami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 33, Application US/10311034; GENERAL INFORMATION:
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BANDMAN, Olga
BOROWSKY, Mark L.
AU-YOUNG, Janice
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US-10-311-034-33
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421 AAGAGCGGAACATATTGTCGGAAGCACAGCCCGTGGATCCCCCAATTACAGTATGCCT 480

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RESULT 3 US-60-215-651-9 ; Sequence 9, Application US/60215651 ; GENERAL INFORMATION:

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APPLICANT: Agee, MICRIEL L.
APPLICANT: Agee, MICRIEL L.
APPLICANT: Bergeh, CONSTANCE
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERRACE: 21402-462C-601
CURRENT PELICATION NUMBER: PCT/US02/31373
CURRENT FILING DATE: 2003-10-01
PRIOR PELING DATE: 2002-10-01
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-03
PRIOR PILING DATE: 2001-10-03
PRIOR PELING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/301,642
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-06-16
PRIOR PELING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2001-10-09
PRIOR PILING
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches
                                                                                                                                                     Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Curagen Corporation
Smithson, Glennda
Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets, Richard A. Rothenberg, Mark E. Leach, Martin D. Agee, Michele L.
                                                                                                                                                                                                                                                                                                                                      Zerhusen, Bryan D. Anderson, David W. Zhong, Mei Catterton, Elina Ji, Weizhen Miller, Charles E. Rastelli, Luca Stone, David J. Pena, Carol E. A. Shenoy, Suresh G.
                                                                                                                                                                                                                                                                                                                        Gorman, Linda
                                                                                                             Ju, Jingfang
Li, Li
                                                                                                                                                                                                                                                                                               Ort, Tatiana
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; LOCATION: (2)..(1870)
PCT-US02-31373-3
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ORGANISM: 268667493
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                                            563
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                                                                                                                           CACTITIGAATAGATAGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 623
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                                                                                        CACTITIGAATAGATATAGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG
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                                          504 Trcaddacaaaarcaccrirarcregrcaregaararcagccregaggggacrregrer
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                                TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
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Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
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Miller, Charles B.
Rastelli, Luca
Stone, David J.
Pena, Carol B. A.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Uu, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sashi
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Anderson, David W.
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Catterton, Elina
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Pred. No. 0;
0; Mismatches
Query Match 93.7%;
Best Local Similarity 99.8%;
Matches 1390; Conservative
                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (2)..(1870)
US-10-262-511-3
                                                                                                                                                                         LENGTH: 1870
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US-10-791-666-3
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         APPLICANT: Shinkets, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele I.
APPLICANT: Agee, Michele I.
APPLICANT: Berghs, Constance
TITLE OF INVENTION NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-4622.
CURRENT APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PLILNG DATE: 2002-06-17
PRIOR PLILNG DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR PLILNG DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PLILNG DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PLILNG DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PLILNG DATE: 2002-06-16
PRIOR APPLICATION NUMBER: 60/331,260
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR PLILNG DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR APPLICATION NUMBER: 60/373,260
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PRIOR PLING DATE: 2002-04-17
PLEMENT PLING DATE: 2002-04-17
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Pred. No. 0;
0; Mismatches
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
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Best Local Similarity 99.8%;
Matches 1390; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (2)
US-10-262-511A-3
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APPLICANT: YILLY Xuanchuan
APPLICANT: Wiranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Fiddle, Carl Johan
TITLE OF INVENTION: Novel Huan Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
FILE REFERENCE: LEX-0289-USA
FILE REFERENCE: LEX-0289-USA
FILE REFERENCE: LEX-0289-USA
FILE REFERENCE: LOS/10/791,666
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6165
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                                                                                                                                                                        GTGACTGGTGGTCAGTGGGCTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG
                                                                                        791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                   1031 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTTAAAATTG
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                                                                                                                                                GTGACTGGTGGTCGGTGGTGGTTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG
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Pred. No. 0;
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US-10-791-666-1
; Sequence 1, Application US/10791666
; GENERAL INFORMATION:
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            APPLICANT: Yu, Xuanchuan
APPLICANT: Wiranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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ORGANISM: homo sapiens
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GENERAL INFORMATION
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TCAAATATGAGGGGGGAATCCTTTGGATGCTGCTGAACCCATTGCCAACCGGG 60   TCAAATATGAGGGGGGGAATCCTTTGGATGCTGCTGCTGACCCATTGCCAACCGGG 60   TCAAATATGAGGGGGGGGAATCCTTTGGATGCTGGTGCTGCTGACCCATTGCCAGCGGG 70   TCAAATATGAGGGGGGGGAAACCCTTTATGACCCATTGCCAGCGGG 70   CCTCCAGGCTGAATCTTTCTCCAGGGAAACCACCCTTTATGACACCATTGCCAGCGGG 70   CCTCCAGGCTGAATCTTCTCCAGGGAAACCACCCTTTATGACACCAGCAGATGT 130   CCTCCAGGCTGAATCTTTCTCAGGGAAACCACCTTTATGAACATGAAGATGT 130   CTCCTCTTTCCCGAGAGGATATAAGAAGCCCTCTTTGTTCTCTTTGAAGAATGCAGT 130   CTCCTCTTTCCCGAGAGGAAATTAAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGT 130   CTCCTCTTTCCCGAGAAGGAAATAAGAAGCACCTCTTTGTTCTTTTGAAGAATGCAGT 130   CTCCTCTTTCCCGAGAAGGAATTAAGAAGCACCTCTTTGTTCTTTTGAAGAATGCACCA 250   CTTTTCTTAAAGAAGAATAAGAAAGCAACCAGAAGTATTTGTCCGAAAGAAA	16.   CTATGANAGTGATGANGAGGGTTTATTGGGCCGGGGAGCAGGTTTCATTTTTTGAGG 17. CTATGANAGTGATGAAGAAGAAGAGGCTTTATTGGCCGAGGAGGAGGAGGTTTCATTTTTTGAGG 18. CTATGAAAGTGATTATCTCGACACACACCCGTGGATCCCCCAATTACAGTATGCT 19. TTCAGGACAAAATCACTTTATCTCGGTCATGGAATCCCCCCAATTACAGTATGCT 19. TTCAGGACAAAATCACCTTTATCTCGGTCATGGAATACCCCCGAATTACAGTATGCT 19. TTCAGGACAAAATCACCTTTATCTCGGTCATGGAATACCCCCCAATTACAGTATGCTT 19. TTCAGGACAAAATCACCTTTATCTCGGTCATGGAATACCAGTACAGTTTACCTAGCTT 29. TTCAGGACAAAATCACCTTAACTGAAAAACCTCAAACACTCAGAACCCCCAATTACATTTACCTAGCTT 29. TTCAGGACAAAATCACACACCACAAACCCAGAAAACCTCAACAGAACCTACACTTTACCTAGCTT 29. TTCAGGACAAAATCAACAAGCACCAGTACAATCAAACAGCTCCAATTAACATTTTACCTAGCTT 20. CACTTTTGAATAGATACAACAAGCACCAATAAACAACTCAACATCAACATTTAACAACAACACTCAACACACACACACACACACACACACACACACACACACAC
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                                                                         905 GIGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 964
     1145 ACTGGAACATCGTAACTCTCCTCCCCCTTCGTTCCTCCTCAAGTCTGACGATG
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; Pred. No. 0;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECT
FILE REFERENCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 7679
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Best Local Similarity 99.8
Matches 1390; Conservative
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ORGANISM: HUMAN
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US-10-170-235-7679
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Pred. No. 0;
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; OTHER INFORMATION: Incyte ID No: 7484498CB1
US-10-415-011-43
                    60/252,730
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/
PRIOR PILING DATE: 2000-11-25
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL PROGram
SEQ ID NO 43
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.8%;
Matches 1390; Conservative
                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 0;
0; Mismatches
; TITLE OF INVENTION: 32838,336 and 52908
; FILE REFERENCE: MPIO1-294PIRNWOM
; CURRENT APPLICATION NUMBER: PCT/USO2/41011
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FBSESEQ for Windows Version 4.0
; SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.5%;
Matches 1386; Conservative
                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(6162)
PCT-USO2-41011-11
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Slos-Santiago, Inmaculada
APPLICANT: Rosenfeld, Julie Beth
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
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US-10-325-430-11

i Sequence 11, Application US/10325430

sequence 11, Application US/10325430

sequence 11, INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Rosenfeld, Julie Beth

ITILE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,

ITILE OF INVENTION: 32838, 336 and 52908

FILE REFERENCE: MPI01-294PIRNM

CURRENT APPLICATION NUMBER: US/10/325, 430

CURRENT PILING DATE: 2002-12-19

PRIOR APPLICATION NUMBER: US 60/341, 953

PRIOR FILING DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FaatSEQ for Windows Version 4.0

SEQ ID NO: 21

SEQ ID NO: 21
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; NAME/KEY: CDS.
; LOCATION: (1).
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                                                                                                                        RESULT 19094-00750-51
Sequence 51, Application PC/TUS0400750
Sequence 51, Application PC/TUS0400750
Sequence 51, Application PC/TUS0400750
GENERAL INFORMATION:
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Infasor, 1985, 1986, 1986, 1986, 1986, 1987, 1987, 1987, 1987, 1986, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987, 1987
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Matches 1386; Conservative
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Sequence 1 Sequence 1 Sequence 1 Sequence 8

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Sequence 1 Sequence 4 Sequence 1

Sequence 116, App Sequence 26, Appl Sequence 26, Appl Sequence 39, Appl Sequence 179, App Sequence 101, Appl Sequence 101, Appli

ALIGNMENTS

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 1, Application US/09804471A
Patent No. US20020132322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT PILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 1481; Conservative
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ORGANISM: Human
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CCCTCTTCCCGAGAAGGGATATTAGACGCACTTTGTTCTTTGTAGAAGATTCGAAGAATTCGAAGACCACACACA	QY         1261         CACTGGGGATTCTTGGTAGATCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA         1320           DD         1277         CACTGGGGATTCTTGGTAGATCTGTTGTTGTGTCGGGTCTGGACTCCCTGCCAAGA         1336           QY         1321         CTAGCTCCATGGAAAGAACTTCTCATCAAAAGCAAAGAGTCTCAGGACA         1380           DD         1337         CTAGCTCCATGGAAAACATTCTCATCAAAAGCAAAAGCTACAAGACTTCAAGGACA         1396           QY         1381         AGTGTCACAAGGTATTATTTCCGCAGCCGGCCTCCTTGCTCCAGGATCTCCCGGT         1440           DD         1397         AGTGTCACAAGGTATTATTTCCGCAGCCGGCCTCCTTGCTCCAGGATCCTCCCGT         1456           QY         1397         AGTGTCACAAGGAATTTATTTTCCGCAGCCGCCTCCTTCCT	RESULT 2 US-10-238-709-1 is Sequence 1, Application US/10238709 is Publication No. US20030022340A1 is GENERAL INFORMATION: is TITLE OF INVENTION: is TITLE OF INVENTION: is FILE REPERENCE: CLOONIG HUMAN KINASE PROTEINS, AND USES is TITLE OF INVENTION: THEREOF is FILE REPERENCE: CLOONIG HUMAN KINASE PROTEINS, AND USES is TITLE OF INVENTION: THEREOF is FILE REPERENCE: CLOONIG HUMAN KINASE PROTEINS, AND USES is TITLE OF INVENTION: THEREOF is CURRENT APPLICATION NUMBER: US/10/238,709 is CURRENT FILING DATE: 2002-09-11 is UBNGTHS: FSSELSEQ for Windows Version 4.0 is SEQ ID NO 1 is LENGTH: 1515 it TYPE: DNA it CORANISM: Human US-10-238-709-1	Query Match         100.0%; Score 1481; DB 14; Length 1515;           Best Local Similarity         100.0%; Pred. No. 0;           Matches 1481; Conservative         0; Mismatches         0; Indels         0; Gaps         0;           Qy         1 TCAAATATGGAGGGGGAATCCTTTGGATGCTGGTGCTGAACCCATTGCCAACCGGG 60         1) TCAAATATGGAGGGGGGAATCCTTTGGATGCTGGTGCTGAACCGTTAAGGGGGAACCGTTGGAGAGGG 76         0           Qy         61 CCTCCAAGGGTGAATCTGTTCTTCCAGGGGAAACCACTTAATGACTGAAACGAGAAGTT 120         0	Db   77	QY         241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG 300           DD         257 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG 316           QY         301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360           DD         317 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360           DD         317 GTTGTCGTCACTTTGCTGAAGTGCTAGATGGTAAGAGAAAAGCAACCGGGGACATCTATG 376           QY         361 CTATGAAAGTGAAGAAAAAAAAAAAAAAAAAAAAAAAAA	377 CTATGAAGTGATGAAGAAGAGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGGGGGGGAGCAGGGTTTCATTTTTTGGGGGGGAGCAGGGTTTCATTTTTTGGGGGGGG
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Publication No. US20040091993A1

GENERAL INFORMATION:

APPLICANT: WESTER, Marion et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOOL164DIV II

CURRENT FILING DATE: 2003-12-02

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PASLESC for Windows Version 4.0

SEQ ID NO 1
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ORGANISM: Homo sapiens
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                                                              CACTITIGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTITIACCTAGCTG
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                TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT
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US-10-724-594-1
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APPLICANT: DOLIGEX, Jennifer L.
APPLICANT: DING, Li
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APPLICANT: DING, Li
APPLICANT: ELLOTT, Vicki S.
APPLICANT: ELLOTT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT APPLICATION NUMBER: G0/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; 60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-07-07; 2000-07-13; 2000-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CB1
US-10-311-034-33
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Pred. No. 0;
0; Mismatches
                                         HAFALIA, April
ARVIZU, Chandra S.
GURURAJAN, Rajagopal
LO, Terence P.
                                                                                                                                                 KHAH, Farrah A.
RECIPON, Shirley A.
AZIMZAI, Yalda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.7%;
Best Local Similarity 99.8%;
Matches 1478; Conservative
HE, Ann
THORNTON, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 2066
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                                                                    GTGACTGGTGGTCAGTGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900
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DB 17; Length 2066;
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GANDHI, Ameena R.
TRIBOULEY, Catherine M.
CHAWLA, Narinder K.
YAO, Monique G.
LU, Dyung Aina M.

APPLICANT: APPLICANT: APPLICANT:

GREENWALD, Sara R. RAMKUMAR, Jayalaxmi GRIFFIN, Jennifer F

NGUYEN, Danniel B. TANG, Y. Tom Neil

APPLICANT: APPLICANT:

BURFORD, KEARNEY

APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BANDMAN, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: AU-YOUNG, Janice
APPLICANT: LU, Yan
APPLICANT: GANDHI, Ameena R.
APPLICANT: CHAMLA, Narinder K.

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Ju, Jingfang
Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
                                                                                                                               Ellerman, Karen
Malyankar, Uriel M.
                                                                                                                                                                   Gorman, Linda
Zerhusen, Bryan D.
Anderson, David W.
               Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
                                                                                                                                                                                                        Zhong, Mei
Catterton, Elina
                                                                                                                                                        Ort, Tatiana
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ORGANISM: Homo sapiens
FEATURE:
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US-10-262-511-3
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                                                                                       601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660
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APPLICANT: Miler (Garles E. APPLICANT: Raiselili, Luca
APPLICANT: Raiselili, Luca
APPLICANT: Retone, David J. APPLICANT: Retone, David J. APPLICANT: Berno, Survesh G. APPLICANT: Berno, Survesh G. APPLICANT: Berno, Survesh G. APPLICANT: Retone, Martin D. APPLICANTON NUMBER: 60/326,443
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PRIOR PRINCE 2002-05-10
PRIOR PRINCE PLING DATE: 2002-05-10
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US-10-262-511-3 ; Sequence 3, Application US/10262511 ; Publication No. US20040038223A1 ; GENERAL INPORMATION:

Publication No. US20040209297A1   GENERAL INFORMATION:   APPLICANT: Wix Xuanchuan   APPLICANT: Wix Xuanchuan   APPLICANT: Wix Xuanchuan   APPLICANT: Wix Maricar   APPLICANT: Wix Maricar   APPLICANT: Friddle, Carl Johan   TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same   FILE REPERENCE: LEX. 2018-0.18   FILE REPERENCE: LEX. 2018-0.18   CURRENT PILING DATE: 2004-03-02   PRIOR APPLICATION NUMBER: US/10/028,946   PRIOR APPLICATION NUMBER: US 60/258,335   PRIOR APPLICATION NUMBER: US 60/258,335   PRIOR PRILING DATE: 2000-12-27   NUMBER OF SEQ ID NOS: 4   SOFTWARE: Fast SEQ for Windows Version 4.0   SEQ ID NO 3   LENGTH: 5877   TYPE: DNA   ORGANISM: homo sapiens	Query Match 93.7%; Score 1388.2; DB 18; Length 5877; Best Local Similarity 99.8%; Pred. No. 0; Matches 1390; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Oy 1 TCAAATATGGAGCGCGAATCCTTTGGATGCTGCTGCTGAACCCATTGCCAACGGG 60	Oy 61 CCTCCAGGCTGAATCTGCTTCTTCCAGGGGAAACCACCCTTATGACTCAACAGCAGATGT 120	Qy 121 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTGAAGAATGCCGTC 180	Oy 181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGGACCA 240	OY 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300  251 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310	QY 301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360	Oy 361 CTATGAAGAGATGAAGAAGAAGCTTTATTGGCCCAGGAGGTTCATTTTTGAGG 420	Oy 421 AAGAGCGGAACATATTATCTCGAAGCCCGTGGATCCCCCAATTACAGTATGCCT 480	Qy 481 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 540	OY 541 CACTITIGAAIAGAIAGAGACCAGIIAGAIGAAAACCTGAIACAGIITITACCIAGCIG 600	601	DD 911 AGCIGATITIGGCIGITCACAGCGITCATCIGATGCGGGCATGAGGTGGATTTTGGATGTGGCGG 720  Qy 661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720	Db 671 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 730
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301 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTAIG 360  311 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTAIG 370  312 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG 370  313 GTTGTGAAAGTGATGAAGAAGAAGACTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG 420  421 AAGAGGGGAACATTATTGCCCAGGAGCAGGTTTCATTTTTTTGAGG 430  421 AAAAGCGGAACATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACGTTATGCCT 480  431 AAAAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAGTATGCCT 480	TTCAGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT 	541 CACTITIGAATAGATATGAGGACCAGTIAGATGAAAACCTGATACAGTITIACCTAGCTG 600 	601 AGCTGATTTTGGCTGTTCACAGCGTTCATGATGGGATACGTGCATCGAGACATCAAGC 660 	661 CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720 	721 CGAAATGAATTCAAACAATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780 	781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGAATGGAAAAGGCACCTACGGCCTGGACT 840 	841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG 900 	901 CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 960 	961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGGCG 1020 	1021 GCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTCTTAAAATTG 1080 	1081 ACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1140 	1141 ACACCTCCAATTTTGATGAACCAGAGAAGAATTGGTGGGTTTCATCCTCCGTGCCAGC 1200 	1201 TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTTCGTACAGCAAGG 1260 	1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTCGGGTCTGGACTCCCCTGCCAAGA 1320	1321 CTAGCTCCATGGAAAGAACTTCTCATCAAAGGAAAGAGCTACAAGACTCTCAGGACA 1380 
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; OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CB1
US-10-415-011-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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93.7%; Score 1388.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANI: SUARANAKER Anitea D.
APPLICANI: SUARANAKER Anitea
APPLICANI: THANGAVELU, Kavitha
APPLICANI: THANGAVELU, Kavitha
APPLICANI: THANGAVELU, Kavitha
APPLICANI: ISON, Craig H.
ITILE OF INVENTION: HUMAN KINASES
FILE REFRENCE: PLO-262 USN
CURRENT APPLICATION NUMBER: US/10/415,011
CURRENT APPLICATION NUMBER: US 0/242,410
FRIOR APPLICATION NUMBER: US 60/242,410
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-110-27
FRIOR FILING DATE: 2000-110-27
FRIOR FILING DATE: 2000-11-03
FRIOR FILING DATE: 2000-11-09
FRIOR FILING DATE: 2000-11-09
FRIOR FILING DATE: 2000-11-09
FRIOR APPLICATION NUMBER: US 60/247,672
FRIOR APPLICATION NUMBER: US 60/247,672
FRIOR APPLICATION NUMBER: US 60/252,730
FRIOR APPLICATION NUMBER: US 60/252,730
FRIOR APPLICATION NUMBER: US 60/252,730
FRIOR APPLICATION NUMBER: US 60/250,807
FRIOR FILING DATE: 2000-11-12
FRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                               TANG, Y. Tom
HAFALIA, April J.A.
NGUYEN, Danniel B.
CANDHI, Ameena R.
LU, Yan
YUE, Henry
BURFORD, Neil
BANDMAN, Olga
TRIBOULEY, Catherine M.
LAL, Preeti G.
RECIPON, Shirley A.
LU, Dyung Aina M.
BOROWSKY, Mark L.
BOROWSKY, Mark L.
                                                                                                                                           Sequence 43, Application US/10415011
Publication No. US20040053394A1
GENERAL INFORMATION:
                                                                                                                                                                                                  APPLICANT: INCYTE CORPORATION
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: BAUGHN, Mariah R.
APPLICANT: CHAWLA, Nariaha K.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: XU, Yuning
APPLICANT: ARVIZU, Chandra S.
APPLICANT: YAO, MONIQUE G.
APPLICANT: YAO, MONIQUE G.
APPLICANT: RAMKUMAR, Jayalaxmi
1381 AGTGTCACAAGGT 1393
                                     AĠrĠrĊAĊAÄĠAr 1403
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ORGANISM: Homo sapiens
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SEQ ID NO 43
LENGTH: 6298
                                     1391
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT
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11	1321 CTAGCTCCATGGAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTTCTCAGGACA 1380 1331 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA 1390 1381 AGTGTCACAAGGT 1393 1391 AGTGTCACAAGAT 1403
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1145	

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720 730 780 790

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Sequence 1, Application US/10017216
Bublication No. US20020160483A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KAPELLER-LIBERMANN, Rosana
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: 10147-5701
CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTION OF: 2.1
SEQ ID NO: 7
SOFTWARE: PALENTIN OF: 2.1
SEQ ID NO: 7
SEQ ID N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1081 ACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG 1140
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                  511 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1201 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACAGCAAGG
                                                                                       CTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGATCTGCCG
                                                                                                                                                 671 creadaacarreregradeeeacacacarcarcaageregragarrregarereee
                                                                                                                                                                                                                             CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCCAGATTACA
                                                                                                                                                                                                                                                                     TGGCTCCTGAAGTGCTGACTGTGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
                                                                                                                                                                                                                                                                                                                                                                                                               GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGGAGATCCCCCTTCG
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RESULT 12
US-10-225-430-11
Sequence 11, Application US/10325430
Fublication No. US2003015352541
Fublication No. US2003015352541
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millense Beth
TITLE OF INVENTION: MAIN PAINTUL DISORDERS USING 1465, 1587, 2146, 2207,
TITLE OF INVENTION: 32838,336 and 52908
TITLE OF INVENTION: MINDER: US/10/325,430
CURRENT APPLICATION NUMBER: US/10/325,430
CURRENT FILING DATE: 2002-12-19
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 21
ENGRENT FALES FastERQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 6162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370
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93.3%; Score 1381.8;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1386; Conservative 0; Mismatches
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ORGANISM: Homo Sapiens
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; LOCATION: (1)...(6162)
US-10-325-430-11
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| Publication No US2003015352A1
| GENERAL INCOMMATION:
| APPLICANT: Millennium Pharmaceuticals, Inc.
| APPLICANT: Silos-Santiago, Inmaculada
| APPLICANT: Silos-Santiago, Inmaculada
| APPLICANT: Sosenfeld, Unle Beth
| TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
| TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207
| TITLE OF INVENTION: MATHODS AND COMPOSITIONS IN TREATING
| TITLE OF INVENTION: A2283 4,336 and 52908
| FILE REFERENCE: MPIOL-294PIRNM
| CURRENT APPLICATION NUMBER: US/10/325,430
| PRIOR APPLICATION NUMBER: US 60/341,953
| PRIOR FILING DATE: 2001-12-19
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 10
| LENGTH: 6574
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Pred. No. 0;
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ORGANISM: Homo Sapiens
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                                                                                                                                                    CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATGACTCAACAGCAGATGT
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                                                      Score 1381.8;
                                                                       Pred. No. 0;
0; Mismatches
                                                    93.3%;
99.5%;
                                                  Query Match
Best Local Similarity 99.5
Matches 1386; Conservative
ORGANISM: Homo sapiens
     ; OKGANISH: m
US-10-017-216-1
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93.3%; Score 1381.8;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1386; Conservative 0; Mismatches
                                                                             1381 AGTGTCACAAGGT 1393
                                                                                                 ; NAME/KEY: CDS
; LOCATION: (19)...(6180)
US-10-757-262-51
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                               TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300
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                                                                                                                GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATG
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QQ	1349 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAAAGACTCTCAGGACA 1408	TCAGGACA 1408
ò	1381 AGTGTCACAAGGT 1393	
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                                                                              March 19, 2005, 07:56:21; Search time 261.498 Seconds (without alignments) 9267.079 Million cell updates/sec
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(cgn2_6/ptodata//ina/5A_COMB.seq:*
(cgn2_6/ptodata//ina/5B_COMB.seq:*
(cgn2_6/ptodata///ina/6A_COMB.seq:*
(cgn2_6/ptodata///ina/6B_COMB.seq:*
(cgn2_6/ptodata///ina/Regi:*
(cgn2_6/ptodata///ina/PcTUS_COMB.seq:*
(cgn2_6/ptodata///ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-2640
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US-08-422-699A-12
US-08-422-699A-8
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US-09-171-156A-20
US-09-004-730A-20
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2 US-08-422-699A-10 2 US-08-422-706B-10 3 US-09-442-100-7 4 US-09-442-100-7 4 US-09-422-106-7 3 US-09-509-902A-15 3 US-09-509-902A-15 4 US-09-233-857-2 5 US-08-860-150-6 3 US-09-233-857-2 5 US-08-872-796-11 5 US-09-272-796-11 5 US-09-442-100-5 6 US-09-442-100-5 6 US-09-442-100-5 7 US-09-442-100-5 7 US-09-248-796A-4400 7 US-09-248-796A-4400 7 US-09-248-796A-4400	ALIGNMENTS	NASE PROTBINS, NCODING HUMAN, 471A	.0%; Score 1481; DB 4; .0%; Pred. No. 0; . 0; Mismatches 0;	CAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGG 	CTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCTTTATGACTCAACAGATGT 	CTCCTCTTTCCCGAGAAGGATATTAGATGCCCTCTTTGTTCTCTTTGAGAATGCAGT 	CTGATGAAGATTAAGGACGTGAGCAACTTTGTCCGGAAGTATTCCGACAC 	CAGCCTTCGGCAAAGGA 	GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 	Ctatgaaagtgatgaagaagagctttattggcccaggagcaggtttcatttttgag
156.4 10.6 3323 125.8 8.5 3155 125.8 8.5 3155 125.4 8.5 1498 125.4 8.5 1961 125.4 8.5 1961 121 8.2 3018 114.6 7.7 1935 113 7.6 3213 113 7.6 3213 110.4 7.5 1213 110.4 7.5 1213 110.4 7.5 1213	•	471A-1 1, Applicati 1, Applicati 1, Applicati 1, Applicati 1, Applicati 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1	100 Similarity 100 I, Conservative	1 TCAAATATGGAGCGCGC              17 TCAAATATGGAGCGCG	61 CCTCCAGGCTGAATCTGTT 77 CCTCCAGGCTGAATCTGTT	121 CTCCTCTTTCCCGAGAA 	181 AGCCTGCTCTGATGAA(                      197 AGCCTGCTCTGATGAAG	241 TAGCTGAGTTACAGGAGCTC 	301 GTTGTGGTCACTTTGC: 	361 CTATGAAAGTGATGAA( 
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                             Sequence 1, Application US/10238709
; Sequence 1, Application US/10238709
; Patent No. 6680188
; GENERAL INFORMATION:
   APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND US FILLE OF INVENTION: THEREOF
; FILLE REFERENCE: CLO01164D1V
; CURRENT APPLICATION NUMBER: US/10/238,709
; CURRENT APPLICATION NUMBER: US/10/238,709
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ FOR WINGOWS Version 4.0
; SEQ ID NO 1
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;; Pred. No. 0;
0; Mismatches
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Best Local Similarity 100.
Matches 1481; Conservative
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                                                                                      TTCAGGACAAAAATCACCCTTTATCTGGTCATGGAATATCAGCCTGGAGGGACTTGCTGT
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US-10-028-946-3
US-10-028-946-3
Sequence 3, Application US/10028946
Fatent No. 6734009
GENERAL INFORMATION:
APPLICANT: Winternan Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polynucleotides Encoding the FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
CURRENT PILING DATE: 2001-12-20
FRIOR PILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 5877
TYPE: DNA
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3 B 3 B 3 B 5 B 5 B 5	6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	6 8 6 8 6 8 6 8 6 8 6
Db 971 TTCCAGATGACCCCAAAGTGACCAGTGACTTCTTGATCTGATCTATGTGCG 1030  Oy 1021 GCCAGAAAGAGACTGAAGTTTGAAGTCTTTGTTGATCTTCTTTTTTTT	0	TYPE: DNA   TYPE

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Sequence 1, Application US/09916204

Patent No. 6638745

GENERAL INFORMATION:

APPLICANT: WEI, MING-Hui et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: 2001-09-24

CURRENT APPLICATION NUMBER: US/09/916,204

CURRENT PILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
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     734 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 793
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                                                                                                                                                                                                854 TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGGCCTGGAGGGGACTTGCTGT
                                                                                                                                                                                                                                                                             CACTITITGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTITACCTAGCTG
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                                                           421 AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAGTATGCCT
                                                                                                              794 AAGAGCGGAACAFATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAGTATGCCT
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0; Mismatches 2;
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Best Local Similarity 99.7%;
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ORGANISM: Human
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APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje T.
ITILE OF INVENTION: No. 6743619el Nucleic Acids and
ITILE OF INVENTION: Polypeptides
ITILE REFERENCE: 802
CURRENT PILICANTON: POLypeptides
FILE REFERENCE: 802
CURRENT PILICANTON: NOWBER: US/09/774,528
CURRENT PILICANTON: APPLICATION NUMBER: US/09/774,528
CURRENT PILICANTON: APPLICANTON: APPLICANT
                                                                                                                                                                                                                                                                    Sequence 419, Application US/09774528
Patent No. 6743619
PAPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodsich, Ryle
APPLICANT: Liu, Chenghua
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
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Matches 949; Conservative
                                                                                  1381 AGTGTCACAAGGT
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US-09-774-528-419
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US-09-949-016-2640

Sequence 2640, Application US/09949016

Sequence 2640, Application US/09949016

Sequence 2640, Application US/09949016

Sequence 2640, Application US/09949016

FRICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERBUCE: CL001307

CURRENT FILING DATE: 2000-04-14

FRIOR APPLICATION NUMBER: 60/231,768

FRIOR PELING DATE: 2000-10-03

FRIOR APPLICATION NUMBER: 60/231,498

FRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2640

LENGTH: 2423

LENGTH: 2423
                                                                                                                  244 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACA 303
     CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 183
                                                                                                                                                                                  TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAAGTCAGAAGTCTTGTAG
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                                                              CTCCTCTTTCCCGAGAGGGATATTAGATGCCCTCTTTGTTCTTCTTTGAAGAATGCAGTC
                                                                                                 181 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA
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CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC 243
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Patent No. 6622948

Patent No. 6622948

Patent No. 6622948

EMERRAL INFORMATION:
APPLICANT: WEI, MIGHUI et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND UTITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOL164CIP-DIV
CURRENT APPLICATION NUMBER: US/10/282,048

NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeQ for Windows Version 4.0
SEQ ID 0.1
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16; Conservative
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ORGANISM: Human
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Best Local Simil
Matches 746; C
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US-10-282-048-1
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                                                      1210 CAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACA 1254
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                                                                                                                                                                                                                                                                                                           APPLICANT: Brook, J. David
APPLICANT: Brook, J. David
APPLICANT: Brow, Duncan J.
APPLICANT: Shaw, Duncan J.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DNA SEQUENCE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                          2098 CIGCALITICIGCCACCALCIGCCALITIGITGGITTIACATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 225.6; DB 2; 54.0%; Pred. No. 5.3e-65; cive 0; Mismatches 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB9202485.0 FILING DATE: 06-FEB-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       Sequence 12, Application US/08422699A Patent No. 5955265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
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Best Local Similarity 54.0
Matches 534; Conservative
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CITY: Lexington
STATE: Massachusetts
COUNTRY: US
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CLASSIFICATION:
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Best Local Similarity 52.5
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APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Braw, Duncan J.
APPLICANT: Harley, Helen G.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DNS-REQUENCE ENCODING THE MYOTONIC
TITLE OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton D.
STREEN
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FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839 PELING DATE:
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MEDIUM TYPE: Floppy
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JMBER: US 08/284,543 08-AUG-1994

GB9202485

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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                             Length 2726;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                             15.2%; Score 225.6; DB 2; ilarity 54.0%; Pred. No. 5.3e-65; Conservative 0; Mismatches 439;
                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REPERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION:
TELEPHONE: 617-861-6240
APPLICATION NUMBER: GB92
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                              2726 base pairs
                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       617-861-9540
                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 534; Conserva
                                                                                                                                                                                                                                                                                                                                  linear
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Sequence 12, Application US/08422706B Patent No. 5977333

RESULT 10 US-08-422-706B-12

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474 TATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGAC 533
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                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 218.8; DB 2;
Pred. No. 1e-62;
0; Mismatches 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: OF-FEB-1993
PRIOR APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: OF-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/GB93/00253
FILING DATE: OF-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/GB93/00253
FILING DATE: OF-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
                                                                                                          ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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ilarity 54.5%;
Conservative
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ATTORNEY/AGENT INFORMATION:
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                             CITY: Lexington
STATE: Massachusetts
COUNTRY: US
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                             423
                                                                               423 TGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGGGAGGTGTCGTGCTTCCGTGAGG 482
                                                                                                                                                                                                                                                                                                             AGGATGAGAACTACCTGTACCTGGTCATGGAGTATTACGTGGGCGGGGACCTGCTGACAC 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               664 AGAACATTCTCGTTGACCGCACAGACACATCAAGCTGGTGGATTTTGGATCTGCCGCGA 723
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                          TGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGGAAG
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                                                                                                                                    AGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCTTTC
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APPLICANT: Brock, J. David

APPLICANT: Housman, David E.

APPLICANT: Housman, David E.

APPLICANT: Harley, Helen G.

APPLICANT: Johnson, Kaith J.

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC

TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCES: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1018 GCGCCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGC----
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Patent No. 5955265
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US-08-422-699A-8
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APPLICANT: Brook, J. David
APPLICANT: Shaw, Duncan J.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
TOWNERS OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1e-62;
0; Mismatches 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERNICE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
                                                                                                                                                                                                 US 08/023,612
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Best Local Similarity 54.5%;
Matches 511; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6892(
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                              26-FEB-1993
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LENGTH: 2511 base pair
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STRANDEDNESS: double
                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE: 26-FEB-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.7%; Score 218.4; DB 1; Best Local Similarity 54.5%; Pred. No. 1.6e-62; Matches 510; Conservative 0; Mismatches 411;
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                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                 TELEX: 762829
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
             713/651-5246
                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                          linear
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                 TELEFAX:
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APPLICANT: Caskey, C. T.
APPLICANT: Fu, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Pizzuti, Antonio
APPLICANT: Penwick, Raymond G.
APPLICANT: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1008 AGCTTGTTGTGCGCCCAGAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGC
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,044
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palace
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019,940
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
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1301 McKinney, Suite 5100
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
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Patent No. 5552282
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ADDRESSEE: Fulbright
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ZIP: 77010-3095
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STATE: Texas
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US-08-484-044-11
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Sequence 3, Application US/10238709
Patent No. 6680188
GENERAL INPORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: TALED MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: TALED MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REPERENCE: CLO01164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
1583 TCCCTTCTTCTTTGGCCTCGACTGGGATGGTCTCCGGGACAGCGTGCCCCCCTTTACACC 1642
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Pred. No. 1e-56;
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                                            1121 CACCCTCAAGTCCGACGATGACACCTCCAATTTTGA 1156
                                                                                         1643 GGATTTCGAAGGTGCCACCGACACATGCAACTTCGA 1678
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100.0%; Pred. No. 10. 10. 0; Mismatches
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LOCATION: (1)...(174493)
OTHER INFORMATION: n = A,T,C or G
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Matches 205; Conservative
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ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) ... (174493)
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ORGANISM: Human
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LENGTH: 174493
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US-09-804-471A-3
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                                                                                                                                  Gaps
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                                                                           Length 174493;
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                                                                              Score 205; DB 4;
Pred. No. 1e-56;
                                                                              Query Match 13.8%; Score 205; DE
Best Local Similarity 100.0%; Pred. No. 1e-
Matches 205; Conservative 0; Mismatches
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Job time : 264.498 secs
; OTHER INFORMATION: n = A,T,C or G US-10-238-709-3
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March 19, 2005, 07:45:41 ; Search time 4489.47 Seconds
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12556.766 Million cell updates/sec
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1481
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GenCore version 5.1.6
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	no	BP146990	AGENCOURT	CR746615	2082-86 M	ax51f11.x	CR746792	ik51b06.y	E0164B04-	E0112C12-	UI-R-BJOp	603280370	OST45249	OST45250	OST417039	1L2-UT007	602014091	BX516291	ul31e08.y	XL068 Bay	UI-R-BJOD	AB0155 Sa	RC5-NT018	IL2-CS004	UI-R-BJOp
-	Description	BP146990	BM904785	CR746615	BG808196	BG944539	CR746792	BQ417810	CN682405	CN678533	BF562826	BI654262	CG501399	CG501400	CG652891	BF380737	BF344814	BX516291	AI882189	CC325092	AW525215	CG869028	BF932611	BF763211	CK841805
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SUMMARIES	ID	BP146990	BM904785	CR746615	BG808196	BG944539	CR746792	BQ417810	CN682405	CN678533	BF562826	BI654262	CG501399	CG501400	CG652891	BF380737	BF344814	BX516291	AI882189	CC325092	AW525215	CG869028	BF932611	BF763211	CK841805
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	Match Length DB	698	1085	492	900	427	485	617	481	479	490	821	449	450	512	340	423	582	521	355	539	336	321	335	524
* Query	Match	40.7	35.2	32.3	29.6	28.6	27.6	27.0	25.7	25.5	22.8	22.3	22.1	21.9	21.5	21.2	21.1	21.1	19.0	19.0	18.8	18.4	18.3	17.7	17.7
	Score	602.6	521.2	478	438.4	423.8	409.4	400.4	380	378	337	329.8	327	325	318.2	314.2	312.8	312.6	281.6	281.4	278.8	272.6	270.8	262.4	262.4
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00000000000000000000000000000000000000	BC008127 CG6557314 CG6557314 BF944809 CF744826 CF744826 CF744826 BC054150 BC05615 BC05615 BY018842 CC1310916 BU475240 BU	ALIGNMENTS  698 bp  1 enriched swir  698 bp  1461  Chordata; Crar Cetartiodactyl  Chordata; Crar Cetartiodactyl  Li, N. and Awata,  XXDOTEN; cons  Eull-length  2 (1), D484-D9  nish;  Ltory, Genome B  Raychologic  Agronish;  C.go.jp	Score Pred.
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10. 1085
/ organism="Homo sapiens"
/ organism="Homo sapiens"
/ organism="Rom"
/ db xref="taxon:9606"
/ clone="IMAGE:5557590"
/ tasue type="melanotic melanoma"
/ lab host="DH10B (phage-resistant)"
/ clone lib="NIH MGC 72"
/ note="Organ: skin; Vector: pcWV-SPORT6; Site_1: NotI;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
Technologies."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                can
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LlAM12279 row: d column: 07
High quality sequence stop: 510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.2%; Score 521.2; DB 5; Best Local Similarity 99.3%; Pred. No. 6.5e-147; Matches 534; Conservative 0; Mismatches 3;
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AGENCOURT_6699306 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557590
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1 (Dases 1 to 1085)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
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           60; Indels
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                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATTGCCAACCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 CCTCCAGGCTAAATCTCTTCTTCCAGGGGAAACCGCCCCTCATGACTCAACAGAGAGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG
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/organism="Mus musculus"
/organism="Mus musculus"
/mol type="mkNA"
/db xref="taxon:10090"
/tissue_type="meural retina"
/dev stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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86.4%; Pred. No. 9.7e-122;
ive 0; Mismatches 76;
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    485 CATGGAAA 492
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                                                                                                        Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14659 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAG998D0712279,
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 110
Fax: +49 30 32639 111
www.rzpd.de
This Glone is available royalty-free from RZPD;
contact RZPD (cloneezzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"

db_xref="taxon:9606"

/clone="INAGP99800712279; INAGE:5557590"

/tissue type="melanotic melanoma"

/lab host="DH10B (phage=resistant)"

/clone lib="NIH MGC 72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: Not1;

Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life
Technologies."
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                   Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P.,
Peters,M., Radelof,U. and Schneider,D.
I.M.A.G.E. cDMs Clone Collection
Unpublished (2004)
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  (bases 1 to 492)
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Query Match 28.6%;
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                              540
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 427)
Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L. Gene expression in proliferating human erythroid cells ganges (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Jeffery L. Miller
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National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9817, National Institutes of Health, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301 402 2373

Tel: 301 402 2373

Fax: 301 435 5148

Email: jm7f@nlh.gov

DNA Sequencing and analyses by National Institutes of Health
Inframural Sequencing Center (NISC).

Plate: 51 row: f column: 11

Seq primer: -21M13 forward primer (ABI).

Location/Qualifiers
161 AGGAGAGGAACATATTATCTCGGAGCACGAGTCCTTGGATCCCCCAGTTACAGTACGCCT
                              TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.nisc.nih.gov/)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ax51f11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="blood"
                                                                                        541 CACTTTTGAATAGATATGAG 560
                                                                                                         BG944539.1 GI:14343911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="unknown"
                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                  sapiens
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
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                                                                                                                                                               RESULT 5
BG944539
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ORIGIN

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CR746792 CR746792 NCI CGAP_Brn64 Homo sapiens CDNA clone IMAGp998E239412; IMAGE:4149886 5', mRNA sequence.
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1 (Dases 1 to 485)

Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E., Peters, M., Radelof, U. and Schneider, D.

I.M.A.G.E. cDNA Clone Collection

Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TITGCTGAAGTGCAGGTGAAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTG
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                                                                                                                                                     1 ccagaaccararracarcccrcrrrcrrcrrrcaacaarccacrcaccrcrc
                                                                                                                                                                                                         192 ATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                        312 TITGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 ATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCTTTCAGGACAAA
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAGD998E239412.
RZPDLIB; I.M.A.G.B. CDNA Clone Collection;
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: 449 30 32639 100
Fax: 449 30 32639 111
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  Length 427;
                                                 Indels
     4;
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Score 423.8; DB 4.
Pred. No. 2.4e-117.
0; Mismatches 2.
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                          Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Scearce (mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 GCTGTGGTCACTTCGCTGAAGTGCAGGTGGNTAGAGAGAAGGCGACCGGGGACGTCTATG 462
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86.0%; Pred. No. 3.9e-110;
iive 0; Mismatches 72;
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                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
             Email: dmelton@biohp.harvard.edu
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 617)
/db_xref="taxon:9606"
/clone="IMAGD998E399412; IMAGE:4149886"
/tissue_type="glioblastoma with EGFR amplification"
/lab host="hlild (Ti phage-resistant)"
/lone lib="NCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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ik51b06.y1 Kaestner ngn3 wt Mus musculus cDNA 5' similar to
TR:088937 088937 RHO/RAC-INTERACTING CITRON KINASE SHORT ISOFORM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGAACCCATTGCCAGCCGGG
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                                                                                                                                                                                                                                                                                                                                                              Length 485;
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Pred. No. 6.3e-113;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                        Query Match 27.6%;
Best Local Similarity 99.8%;
Matches 410; Conservative (
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Sharov,A.A., Plao,Y., Matoba,R., Dudekula,D.B., Qian,Y., Vanburen, V., Falco,G., Martin,P.R., Stagg,C.A., Bassey,U.C., Vanburen, V., Falco,G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kinber,M.L., Yoshikawa,T., Jazadac,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L., Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A., Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A., D'Urso,M., Kelso,J., Hide,W. and Ko,M.S.

Transcriptome analysis of mouse stem cells and early embryos Contact: Dawood B. Dudekula
E0164B04-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04 IMAGE:30782511 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0164 row: B column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="niaEST:E0164B04-5"
|db_xref="taxon:10090"
|clone="NIA:E0164B04 IMAGE:30782511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/EvTac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                        Mus musculus (house mouse)
                                                            CN682405
CN682405.1 GI:47448856
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                                                                                                                                          Mus musculus
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POLYA=No.
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AUTHORS
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JOURNAL
COMMENT
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PEATURES

ORIGIN

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. B. 1 (bases 1 to 479)

B. 1 (bases 1 to 479)

B. Ancov, A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., VanBuren, V., Falco, G., Hamatani, T., Alba, R., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Azadat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlesinger, D., Keller, J., Klunath, T., Hogan, B.L., Curci, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

Transcriptone analysis of mouse stem cells and early embryos PLOS Biol. 1 (3), 410-419 (2003)
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                                                                                                                                                                                                                                                                                           61 GGCGACCGGGGACGTCTATGCCATGAAAATCATGAAGAAGAAGGCTTTGCTGGCCCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                461 CCCCCAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 GCCTGGAGGGGATTTGCTGTCGTTCTGAACAGATACGAGGACCAATTAGATGAGAGCT
                                                                                                                               281 CGAAGTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAA
                                                                                                                                                                                             1 CGAAGTTCGAAGCCTTGTGGGCTGTGGTCACTTCGCTGAAGTGCAGGTGGTTAGAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                   401 GCAGGTTTCATTTTTGAGGAAGAGGGGAACATATTATCTCGAAGCACAAGCCCGTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CCCCCAGTTACAGTAGGCCTTTCAGGACAAAAATAACCTTTACCTGGTCATGGAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 GCCTGGAGGGGACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 TGTGCATCGAGACATCAAGCCCGAGAACATCCTCATCGACCGGACGGGACACATCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 GGTGGATTTTGGATCTGCCGCGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 GGTGGATTTTGGATCAGCCGCTAAGATGAATTCAAATAA---GGTGGATGCCAAACTCCC
                                                                                                                                                                                                                                                          341 AGCAACCGGGGACATCTATGCTATGAAAGTGAAGAAGAAGAAGAAGGCTTTATTGGCCCAGGA
                                                                    Gaps
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Plate: E0112 row: C column: 12
Seq primer: M13 Reverse
High quality sequence stop: 479
                                                                    3;
   Length 481;
                                                                 Indels
   Score 380; DB 7; L
Pred. No. 5.9e-104;
O; Mismatches 55;
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Mus musculus (house mouse)
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CN678533.1 GI:47444984
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Query Match 25.7%;
Best Local Similarity 88.0%;
Matches 426; Conservative
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/ db xref="taxon:10116" |
/clone="UI-R-BJ0p-aip-b-06-0-UI" |
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/dev stage="adult" |
/lab_host="DH108 [Life Technologies] " |
/lab_host="DH108 [Life Technologies] " |
/clone lib="UI-R-BJ0p" |
/clone lib="UI-R-BJ0p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
728, 319 335 8250
Fax: 319 335 8256
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through her I.M.A.G.E. Consortium at
LLNL (info@inage.llnl:gov). IMAGE ID= 1797673
Seq primer: M13 Forward.
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760
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UI-R-BJOp-aip-b-06-0-UI.rl UI-R-BJOp Rattus norvegicus CDNA clone
UI-R-BJOp-aip-b-06-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 490)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
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Rattus norvegicus
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BF562826.1 GI:11672556
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Best Local Similarity 85.3%
Matches 376; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGCGACCGGGGGACGTCTATGCCATGAAAATCATGAAGAAGAAGAAGGCTTTGCTGGCCCAGGA 120
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                                                                                                                                                                                                                                 clone="NIA: B0112C12 IMAGE: 30777539"
                                                                                                                                                                                                                                                                                     /tissue type="Embryonic Stem Cell"
/cell line="129.3 ES cells"
/lab_host="DH108"
                                                                                                               /mol_type="mRNA"
|srrain="1285V|Ev7ac"
|db_xref="niaES":E0112C12-5"
|db_xref="taxon:10090"
                                                                                    organism="Mus musculus"
                                 ocation/Qualifiers
                                                                                                                                                                                                                                                               /sex="Male"
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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (Bases I to 449)

E. (Bases I to 449)

E. Abbuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddla, C.J., Gupta, A., Hansen, G., Hu, Y., Huangy, W., Jaing, C., Key, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.

Whk! kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Contact: Zambrowicz BP

OmniBank
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                                                                                                                                                                  Conservative
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
                                                              CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCTTTTATGACTCAACAGCAGATGT 120
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11 (bases 1 to 821)
12 (bases 1 to 821)
13 (bases 1 to 821)
14 (mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CCTCCAGGCTAAATCTCTTCTTCCAGGGAAACCGCCCCTCATGACTCAACAGAGAGTGT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llhl.gov
Plate: LLAM1786 row: 1 column: 17
High quality sequence stop: 648.
                                                                                                                                                                                                                                                                                                     TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
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/clone="IMAGE:5310496"
/tissue_Ypp="tumor, gross tissue"
/dev stage="5 months"
/lab_host="DH108"
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/strain="NMRI"
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B1654262.1 GI:15568498
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Library constructed by Life Technologies. Investigators providing samples: Lothar Henhighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 ATGCTATGAAAGTGATGA-AGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTT 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 CGCCTTTCAGGACCAAAAATAAACTTTACCTGGTCATGGACACTATCAGCCTGGATGG 655
                                                                                                                                                                                                                                                                                                                          117 TCAAGTATGGTGTGCGGAACCCGCCGGAGGCCAGTGCCTCCGAGCCCATTGCCAGTCGGG
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8
                                                                                                                                                            Length 821;
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                                                                                                                                                         22.3%; Score 329.8; DB 4;
84.2%; Pred. No. 1.5e-88;
ive 0; Mismatches 77;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 450)
S Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Fliggott,J., BeltrandealRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Whal kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Droc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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                            Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9,392(6676):608-11) Class: Gene Trap.

Location/Qualifiers
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1000 Research Forest Drive, The Woodlands, TX 77381, USA
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                                                                                                                                                                           /db xref="taxon:10090"
/clone="0ST45249"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                          /organism="Mus musculus"
                                                                                                                                           /mol_type="mRNA"
/strain="129Sv/Ev"
                    Email: materials@lexgen.com
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512 bp mRNA linear GSS 02-OCT-2003
OST417039 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST417039,
CG652891
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Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
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Zambrowicz, B. P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Guptea, A., Hansen, G., Huyr, Huang, W., Jaing, C., Rey, B. W. Jr., Kipp, P., Kohlhauff, B., Ma.Z. -Q., Markesich, D., Payne, R., Van, Sligtenhorst, I., Vogel, P., Kohrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Zhu, Q., Person, C. and Sands, A.T.

Whill kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
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Best Local Similarity 91.7%; Pred. No. 3.5e-87;
Matches 343; Conservative 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="0ST45250"
/clol_type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/Ev"
                                                                                                                                                                                                              1. .450
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                                                                  Location/Qualifiers
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Mus musculus
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Query Match 21.2%;
Best Local Similarity 97.6%;
Matches 319; Conservative
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1. (bases 1 to 340)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                   Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
mail: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
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Shotgun sequencing of the human transcriptome with ORF expressed
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   Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 318.2; DB 9; Length 512;
Pred. No. 4.4e-85;
0; Mismatches 29; Indels 1;
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/clone_lib="Mus musculus 1295v/Ev"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="OST417039"
                                                                                                                                                                                                                                        Class: Gene Trap.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="129Sv/Ev"
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-UT0073-170900-167-H01&t3=2000-09-17&t4=1)
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                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 TTTTGGGGTCTTTGCTGCCATCCTTTCTTCTCTAAAATTGACTGGAACAACAACATTCGTAAC
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Location/Qualifiers
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/mol_type="mRNA"
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

March 19, 2005, 06:24:41 ; Search time 749.892 Seconds
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11691.196 Million cell updates/sec Run on:

US-10-724-594-1\_COPY\_17\_1497

1481 1 tcaaaatatggagcgcggaat........cccggggccgctgctggctc 1481 score: Sequence: Perfect

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04:\* Database :

geneseqn2003cs:\*geneseqn2003ds:\*geneseqn2004as:\*geneseqn2004bs:\* geneseqn2001as:\*geneseqn2001bs:\*geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aca61394 cDNA enco	Aad59938 Human kin	Ado40591 Human kin	Abz68726 Nucleotid	Aad26454 Human kin	Abz68725 Nucleotid	Ada05643 Human NOV	Abq78871 Human kin		Abq78870 Human kin	Aal55214 Human CRI	Aad38864 Human kin	Aal55215 Human CRI	Adn62808 Human NOV	Adf60993 ORF of pa	Aad39191 Human MDP	Adf60992 Pain asso	Adq89099 Hūman uro	Aas06701 Polynucle	Adj96544 Human cit
SUMMARIES	ΩI	ACA61394	AAD59938	ADO40591	ABZ68726	AAD26454	ABZ68725	ADA05643	ABQ78871	AAL55217	ABQ78870	AAL55214	AAD38864	AAL55215	ADN62808	ADF60993	AAD39191	ADF60992	ADQ89099	AAS06701	ADJ96544
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## ALIGNMENTS

Human; ss; gene; gene therapy; kinase; antisense. 1. .6 /\*tag= a /\*tag= b /product= "Kinase" 1501. .1515 /\*tag= c cocation/Qualifiers cDNA encoding novel human kinase. ACA61394 standard; cDNA; 1515 BP. 11-SEP-2002; 2002US-00238709 13-MAR-2001; 2001US-00804471 (first entry) US2003022340-A1. Homo sapiens. 30-JAN-2003. 11-AUG-2003 ACA61394; Key 5'UTR 3'UTR RESULT 1 ACA61394 CDS 

(APPL-) APPLERA CORP.

Beasley EM; Di Francesco V, Webster M, Yan C,

WPI; 2003-438978/41. P-PSDB; ABU10126.

New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.

796

780

856 900 916 960 1020 1036 1080 1096 1140 1200 1216 1260 1276 1336 1380 1396 1456

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1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTTCGGGTCTGGACTCCCCTGCCAAGA 1320
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                              The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic proteins, and serve as targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic groteins, and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in biological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The mucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for monitoring the effectiveness of modulating compounds on the expression or activity of the transporter gene in clinical trials or in treatment regimen, in gene therapy and as antisense constructs to control transporter gene expression in cells, tissue and organisms. The present
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Best Local Similarity 100.
Matches 1481; Conservative
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kinase related disorder, human, chromosome 12; gene; ss.
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Length 1515;

DB 12;

Query Match 100.0%; Score 1481; Best Local Similarity 100.0%; Pred. No. 0; Matches 1481; Conservative 0; Mismatches

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The present sequence encodes a human citron rho/rac-interacting kinase-short kinase polypeptide. The polymucleotide and polypeptide of the invention are useful in preventing, ameliorating, or treating diseases associated with the polypeptide dysfunction. The expression vector or the reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase-short kinase in a disease, such as obesity or chronic obstructive pulmonary disease. These may also be used for treating obesity/ overweight-associated comorbidities, such as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced fertility, and depression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT 840
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 1479; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
                                                                                                                                                                                                                                                                                                                                                            CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGAGCTACAAAGACTCTCAGGACA
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                                                                                                                                                                                                                                                                         CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTCGGACTCCCCTGCCAAGA
                        ACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCGTGCCAGC
                                                                     ACACCTCCAATTTTGATGAACCAGAGAATTTCGTGGGTTTTCATCCTCTCTGGGCAGC
                                                                                                                        TGAGCCCCTCAGGCTTCTCCGGGTGAAGAACTGCCGTTTTGTGGGGGTTTTTCGTACAGCAAGG
                                                                                                                                                                                                                           CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
                                                                                                                                                                                                                                                                                                                              CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of citron rho/rac-interacting kinase-short kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 1494
//tag= a //product= "citron rho/rac-interacting kinase-short kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; citron rho/rac-interacting kinase-short kinase; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chronic obstructive pulmonary disease; hypertension; diabetes; coronary artery disease; hyperlipidaemia; stroke; gallbladder gout; osteoarthritis; sleep apnea; cancer; thrombolic disease; polycystic ovarian syndrome; fertility; depression; gene; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1497
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2001US-0337130P.
2002US-0375015P.
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/\*tag= a /product= "Human PKIN-7 protein"

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AAD26454 standard; cDNA; 2066
                   (first entry)
                          Human kinase PKIN-7 cDNA.
                   26-MAR-2002
             AAD26454;
  RESULT
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Human, kinase, PKIN-7; cancer; leukaemia, adenocarcinoma, osteoarthritis; munue disorder; atherosclerosis, Crohn's disease; Hodgkin's disease; Acquired disorder; atherosclerosis, Crohn's disease; Hodgkin's disease; anaemia; allergy, asthma, adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mollitus; osteoporosis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; cardiovascular disease; hypertension; vasculitis; myocarditis; osteoporis; congestive heart failure; ischemich heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy; ss.

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Key
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Homo sapiens

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The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition associated with decreased expression of reating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorder include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, melano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.
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Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;
Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
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0; Mismatches
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2000US-0213467P.
2000US-0215651P.
2000US-021605P.
2000US-0218372P.
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Best Local Similarity 99.8%;
Matches 1478; Conservative
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short kinase polypeptide. The polynucleotide and polypeptide of the
invention are useful in preventing, ameliorating, or treating diseases
associated with the polypeptide dysfunction. The expression vector or the
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1224 TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTTCGTACAGCAAGG
                                                                                                                                  CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAAGAGCTACAAAGACTCCTCAGGACA
                                                CACTGGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
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                                                                                                                                                                                 Nucleotide sequence of citron rho/rac-interacting kinase-short kinase.
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/*tag= a
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02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
09-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
15-OCT-2001; 2001US-0329144P.
17-OCT-2001; 2001US-0339169P.
18-OCT-2001; 2001US-0339168P.
24-OCT-2001; 2001US-034965P.
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25-OCT-2001; 2001US-034965P.
26-OCT-2001; 2001US-034965P.
27-OCT-2001; 2001US-034965P.
28-OCT-2001; 2001US-034965P.
17-APR-2002; 2002US-034957P.
                                                                                                                                                       19-APR-2002; 2002US-0373815P.

19-APR-2002; 2002US-0373815P.

19-APR-2002; 2002US-0373817P.

19-APR-2002; 2002US-037384P.

22-APR-2002; 2002US-0374977P.

16-MAY-2002; 2002US-0381037P.

16-MAY-2002; 2002US-0381042P.

17-MAY-2002; 2002US-0381642P.

28-MAY-2002; 2002US-0381642P.

29-MAY-2002; 2002US-0381642P.
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01-OCT-2002; 2002US-00262511
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## (CURA-) CURAGEN CORP.

Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Bisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. P-PSDB; ADA05644.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

## Claim 20; Page 100; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising a polypeptide described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (7) methods for determining the binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above collypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an abstrant expression or above; (10) a method for identifying a potential therapeutic agent for a creening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) a method of a pathology associated with the bolypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating cor preventing a pathology associated with the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian immunian

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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly Ottron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides may have a use in gene therapy. The encoded novel polymeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence encodes a novel human kinase of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 93.7%; Score 1388.2; DB 6; Length 5877; Best Local Similarity 99.8%; Pred. No. 0; Matches 1390; Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                 Disclosure; Page 44-45; 50pp; English.
Miranda M, Friddle CJ;
                                                 2002-599796/64
                                                                        P-PSDB; ABB81928
                                                                                                                                                                                                       applications.
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Citron rho-interacting kinase; gene therapy; mental disorder; cancer;
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citron rho/rac-interacting kinase polypeptide. The isolated a number of citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the polynucleotide and polynucleotide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obseity-associated comorbidities (e.g. hypertension, coronary artery and obseity-associated comorbidities (e.g. hypertension, coronary artery cancer including endometrial, breast, prostate and colon cancer), ancieta, anxiety disorders, prakinson's disease or Alzheimer's disorders, anxiety disorders, Parkinson's disease or Alzheimer's cancerated pain associated with the disorders. These can disorder to treat pain associated with the disorders. The human CRIK polypeptide is also useful in disgnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary cases. The fusion protein is useful for generating antibodies against a central is polypeptide and for use in various assay systems. The modulating are in various assay systems. The column cancer is a column of the case is associated by an expression and disorders or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a contract of the capture of th

New human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or

2001US-0301841P. 2001US-0338651P. 2002US-0375014P.

11-DEC-2001; 25-APR-2002; 02-JUL-2001;

28-JUN-2002; 2002WO-EP007156

WO2003004523-A1

16-JAN-2003

encoding a human

polynucleotide

an isolated

The invention relates to

Disclosure; Page 217-222; 237pp; English

Alzheimer's disease.

WPI; 2003-221576/21

(FARB ) BAYER AG

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useful in producing and detecting the polynucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This polynucleoside sequence represents a DNA sequence relating to the human CRIK protein of the invention

Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;

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TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG
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93.7%; Score 1388.2; DB 9; Length 6156; 99.8%; Pred. No. 0;
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                      Best Local Similarity 99.8 Matches 1390; Conservative
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AAL55217 standard; DNA; 6156

RESULT 9

(first entry)

01-MAY-2003

AAL55217;

diabetes; pain; ds Homo sapiens

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                                                                                                                                              CTATGAAAGTGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG
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The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly Citron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence encodes a novel human kinase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic;
Citron rho-interacting kinase; gene therapy; mental disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, in therapy of disorders and diseases e.g. cancer and pharmacogenomic
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/standard_name= "Single nucleotide polymorphism"
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/product= "Kinase"
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P-PSDB; ABB81927.
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                                                                                                                                            CACTGGGGATTCTTGGTAGATCTGAGGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
                                                                                                      TGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCGTACAGGAAGA
               ACACCTCCAATTTTGATGAACCAGAGAAGTTTCGTGGGTTTCATCCTCCGTGCCAGC
                                   1151 ACACCICCAAITITGAIGAACCAGAGAAGAAITICGIGGGITICAICCICCICCGIGCCAGC
                                                                            TTCGTACAGCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human citron rho/rac-interacting kinase (CRIK) polypeptide polynucleotide, useful in preventing, ameliorating or treating associated with human CRIK dysfunction, e.g. obesity, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CRIK encoding DNA sequence, SEQ ID No 1.
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11-DEC-2001; 2001US-0338651P.
25-APR-2002; 2002US-0375014P.
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perinteation. The fundan circuit and preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obsesty-associated comorbidities (e.g. hypertension, coronary artery and obsesty-associated comorbidities (e.g. hypertension, coronary artery cancer including endometrial, breast, prostate and colon cancer; anortery disease, hyperlipidaemia, stroke, gout, osteoarthitis, some types of cancer including endometrial, breast, prostate and colon cancer).

Concerta, carchexta, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polymucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This polymucleotide sequence represents a DNA sequence encoding a human CRIK protein of the invention
citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK)
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Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;

540 120 CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCTTTATGACTCAACAGCAGATGT 130 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTC 190 240 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 310 430 480 AAGAGGGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCT 490 9 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTC 180 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGGTCAGAAGTCTTGTAG 300 GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG 360 370 CTATGAAAGTGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420 550 CACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600 610 670 20 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGGACTTGCTGT CTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG AGCTGATTTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC rcabarardeadececedaarecrrregarecreerecreereadecearrecageceee CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACACA GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG CTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGG AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAGTATGCCT TTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAACCCCATTGCCAACCGGG Gaps Length 6165; ô 3; Indels Score 1388.2; DB 9; Pred. No. 0; 0; Mismatches 93.7%; 99.8%; Conservative Similarity Query Match Best Local Simil Matches 1390; ( 5 7 61 71 121 131 181 191 241 251 311 371 431 541 551 601 301 361 421 481 491 ద ò g g 셤 ð g 셤 a 셤 ò ò 8 8 ∂ ò ò ద ò 8

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The proteome of a tissue or cell type. PKIN DNA is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN DNA is useful for creating chockin humanised animals or transgenic the proteome of a tissue or cell type. PKIN DNA is useful for creating chockin humanised animals or transgenic the proteome of a tissue or cell type. PKIN DNA is useful for creating chockin humanised animals or transgenic the proteome of a tissue or cell type. PKIN DNA is useful for creating chockin humanised animals or transgenic the proteome of a tissue or cell type. PKIN DNA is useful for creating and in somatic or germline gene therapy. The present sequence is human
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Pred. No. 0;
0; Mismatches
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A, Ison CH;
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27-OCT-2000; 2000US-0244068P.
03-NOV-2000; 2000US-0245708P.
09-NOV-2000; 2000US-0247672P.
16-NOV-2000; 2000US-024565P.
22-NOV-2000; 2000US-0252730P.
01-DEC-2000; 2000US-0259
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Best Local Similarity 99.8%;
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Thangavelu K, Khan FA,
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P-PSDB; AAE24150.
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Homo sapiens
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11-DEC-2001; 2001US-0338651P.
25-APR-2002; 2002US-0375014P.
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                                                                                 CACTGGGGATTCT
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polypeptide is also useful in diagnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polymucleotide and polypeptide and in screening for agents that modulate the activity of the human CRIK polypeptide. This polymucleotide sequence represents a DNA sequence relating to the human CRIK protein of the invention
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0; Mismatches
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99.8%;
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Best Local Similarity 99.8
Matches 1390; Conservative
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Dipippo VA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 3; 395pp; English.
15-OCT-2001; 2001US-0329414P.
17-OCT-2001; 2001US-0330192P.
22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0343059P.
24-OCT-2001; 2001US-0343659P.
29-OCT-2001; 2001US-0343659P.
29-OCT-2001; 2001US-0343659P.
17-APR-2002; 2001US-034365P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
16-MAY-2002; 2002US-0373816P.
16-MAY-2002; 2002US-0373816P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0381845P.
28-MAY-2002; 2002US-0381831P.
25-JUN-2002; 2002US-038135P.
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PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
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EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
AGEE M L.
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ANDERSON D W.
                                                                                                                                                                                                                                                                              SMITHSON G.
MILLET I.
PEYMAN J A.
KEKUDA R.
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CATTERTON E.
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(LILL/)
(GUOX/)
(PATT/)
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     CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGGCTACAAGACTCTCAGGACA 1390
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                GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG
                                                                  CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT
                                                                                                  TTCCAGATGACCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG
                                                                                                                                                                            GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTAAAATTG
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   GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGATCCCCCTTCG
                                                   CAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT
                                                                                                                           Trccagardaccccaaagraagcagraacrrrrcrrgarcrgarrcraaagcrrgragg
                                                                                                                                                  GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTAAAATTG
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05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0327917P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328046P.
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C NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polymucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or activity of NOVX by supplementing the patient our conformal and panes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitete the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify mediators in the production of antibodies and in assays to identify may also be used as anti-NOVX polypeptide antibodies, agonists and artagonists may also be used to medulate NOVX polymucleotide expression and activity of NOVX. polypeptides anti-NOVX polypeptide antibodies, agonists and artagonists may also be used diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotide may be used in this way to prevent, diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and reat: metabolic disorders, dispersed and reat: metabolic disorders, dispersed and disorders, and the various dyslipidaemias, metabolic disturbances associated with chronic diseases and various cancer. Concervances and disorders and the various dyslipidaemias, metabolic disturbances associated with chronic diseases and various cancer. They may also be used as and reading a mine and activity the metabolic syndrome and concern concerns. The metabolic syndrome and activity of NOVX polypediaes and polymediated with chronic diseases and various cancers. represents DNA encoding a human NOVX protein. 8599999999999999999999999

Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;

120 180 240 CCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAACAGCAGATGT 143 203 | TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG 300 360 480 540 263 323 383 CTATGAAAGTGAAGAAGAAGGCTTTATTGGCCCCAGGAGCAGGTTTCATTTTTGAGG 420 503 563 9 83 443 CACITITGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 600 623 CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTC CACTITICAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG 24 rcharardeadcecedaarccirigaarecreerecreereadcearccarreceaeceee CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT CTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAAGAATGCAGTC AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA TGACTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGACATCTATG GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGGAAAGCAACCGGGGACATCTATG CTATGAAAGTGAAGAAGAAGACTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG AAGAGCGGAACATATTATCTCGAAGCCACAAGCCCGTGGATCCCCCAATTACAGTATGCCT TCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGAACCCATTGCCAACCGGG AAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAGTATGCCT TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT Gaps ô DB 12; Length 1870; Indels 5, 93.5%; Score 1385; Clarity 99.6%; Pred. No. 0; Conservative 0; Mismatches Query Match Best Local Similarity Matches 1388; Conserv 61 84 121 181 241 264 324 384 444 541 564 144 204 301 361 421 481 504 g ò g 셤 õ ò 8 ò g 8 6 ò 셤 셤 ò ò 셤 ð

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Unclassified.
1 (bases 1 to 1515)
1 (bases 1 to 1515)
Webster,M., Yan,C., Di Francesco,V. and Beasley,E.M.
Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
Patent: US 6479269-A 1 12-NOV-2002;
Patent: US 6479269-A 1 12-NOV-2002;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
          TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG
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Incyte Genomics, Inc. (US)
Location/Qualifiers
1. 2006
//raganism="Homo sapiens"
//mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 33 from Patent WO01096547.
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1331 CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTTCTCGAGACA
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   791 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
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Regulation of human citron rho/rac-interacting kinase Regulation of human citron rho/rac-interacting kinase Patent: WO 03004523-A 8 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
1. 6156
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                       Yu,X., Miranda,M. and Priddle,C.J.

Human kinases and polynucleotides encoding the same
Patent: WO 02059325-A 3 01-AUG-2002;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
1. 5877
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 0;
0; Mismatches
              Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                               93.7%;
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Best Local Similarity 99.8
Matches 1390; Conservative
 Homo sapiens
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61 CCTCCAGGCTGAATCTTTCCAGGGAAACCACCCTTTATGACTCAACAGCAGATGT 120	TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCATGTAG GTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAAGCAACCGGGGACATCTATG	361 CTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 420	481 TTCAGGACAAAATCACCTTTATCTGGTCATGGAATTATCAGCCTGGAGGGGACTTGCTGT 540	601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC 660 	661 CTGAGAACATTCTCGTTGACCGCACAGACACATCAAGCTGGTGGATTTTGGATCTGCCG 720 	721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACCCCAGATTACA 780 	781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCTGGAACT 840 	841 GTGACTGGTGGTGATGGGGGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG 900 	901 CAGAGGGAACCICTGCCAGAACCTTCAATAACATTATGAATTTCCAGGGTTTTTGAAAT 960 	961 TTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATTCAATTCAAAGCTTGTTGTGCG 1020 	1021 GCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTCTAAAATTG 1080 	1081 ACTGGAACAACATTCGTAACTCTCCTCCCCTTGGTTCCCACCCTCAAGTCCGACGATG 1140 

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                        TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eulbaria; Primates; Catarrhini; Hominidae; Homo
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Regulation of human citron rho/rac-interacting kinase Patent: WO 03004523-A 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
1. .6165
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 0;
0; Mismatches
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Sequence 1 from Patent WO03004523.
AX671105
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Best Local Similarity 99.8%;
Matches 1390; Conservative (
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Qy 241 TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCTTGTAG	301	Qy 361 CTATGAAAGTGATGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTGAGG 	OY 421 AAGAGGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAGTATGCT 	Qy         481         TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT           Db         545         TTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGT	Qy 541 CACTITIGAATAGATATGGGACCAGTTAGATGAAAACCTGATACAGTTTTACCTAGCTG	Qy 601 AGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGACATCAAGC	Qy 661 CTGAGAACATTCTCGTTGACCGCACAGACACATCAAGCTGGTGGATTTTGGATCTGCCG Db 725 CTGAGAACATTCTCGTTGACCGCACAGGACATCAAGCTGGTGGATTTTGGATCTGCCG	Qy 721 CGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGGATTGGGACCCCAGATTACA 	Oy 781 TGGCTCCTGAAGTGCTGACTGTGATGAAGGGGATGGAAAGGCACCTACGGCCTGGACT	Qy 841 GTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTATGGGAGATCCCCCTTCG	Qy 901 CAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGGTTTTTGAAAT 	Qy 961 ITCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG Db 1025 ITCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGCTTGTTGTGCG	Qy 1021 GCCAGAAAGAGACTGAAGTFTGAAGGTCTTTGCTGCCATCCTTTCTTCTAAAATTG 1085 GCCAGAAAGAGAGAGACTGAAGTTTTGCTGCCATCCTTTCTTCTCTAAAATTG	Oy 1081 ACTGGAACAACATTCGTAACTCTCCCCCCTTCGTTCCCACCCTCAAGTCCGACGATG	QY         1141         ACACCTCCCAATTTTGATGAACCAGAGAAGAATTCGTGGGGTTTCATCCTCCGTGCCAGC           Db         1205         ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCTCTCT	Qy         1201         TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTTCGTACAGCAAGG           Db         1265         TGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCGTACAGCAGGAGGAGAAGGAAG	Oy 1261 CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA
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KNSWVSSSPCQLSPSGFEGELCHPFSKIDWNNIRNSPPPFVPTLKSDDDTSNPDEPE
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AY257469 BE16 bp mRNA linear PRI 23-APR-2003 Homo sapiens rho/rac-interacting citron kinase (CIT) mRNA, complete
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RSPEHQPSAMSLLAPPSSRRKESSTPEEFSRRLKERMHHNIPHRFNVGLNMRATKCAV
CLDTVHFGRQASKCLECQVMCHPKCSTCLPATCGLPAEVATHFTEAFCRDKMNSPGLQ
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SHLPAQPDISPNIFEAVKGCHLFGAGKIENGLCICAAMPSKVVILRYNENLSKYCIRK
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RWYTALESVVAGGRVSREKAEADAKLLGNSLLKLEGDDRLDMNCTLPFSDQVVLVGTE
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Matches 1390; Conservative
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Db 131 GAAAT 1023	DD 191 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGGAAGTATCCGACACCACGAGAAGTATCCGACACCACCACGAAGTATCCGACACCACCACACCACACCACACCACACCACACCACACCACA	AATTG 1080 Qy 241	Oy 30.1 GTTGTGGTCAAAGTGCAAGTGCAAAGAGAAAGAAAAGAA			132	138		Qy         661         CTGAGAACATTGACGGCACACATCAGGTGGATTTTGGATCTGCCG         7.20	DNA linear PAT 27-MAR-2003 Qy 721 CGAAAATGAATTCAAACAAGATGCTGAAATCCCGAATTGGGACCCCAGATTACA 780	Qy         781 TGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTACGGCCTGGACT 840	841 GIGACIGGICAGICAGGCGIGAITGCCIAIGAGAIGAITIAIGGGAGAICCCCTICG 90	DD 851	OY 961 TTCCAGATGACCCCCAAAGTGAGCAGTGATTCTTGATTCAAAGCTTGTGGG 1020	.2; DB 6; Length 8603; 09 1021 GCCAGAAAGAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCATCCTTTCTTCTTAAAATTG 1080 0, Db 1031 GCCAGAAAGAGAGACTGAAGTTTGAAGTTTTGCTGCCATCCTTTCTTCTTCTTCTTAAAATTG 1090 1031 GCCAGAAAAGAGAGACTGAAGTTTGAAGTTTTGCTGCCATCCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	60	120 Oy 1141 130 Db 1151	מו טבטעט
CAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGGGTTTTTT	ttccagatgacccaaagtgagcagtgactttcttgatctgattgaagcttgtt 	GCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTCTAA 	ACTGGAACATTCGTAACTCTCCTCCCCCTTCGTTCCCACCCTCAAGTCCGA 	ACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGGTTTCATCCTCCGTGCCAGC 	TGACCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTTCGTACAGG	CACTGGGGATTCTTGGTAGATCTGAGTTGTGTGGGGGTCTGGACTCCCCCCCC	CTACCTCCATGGAAAAGAACTTCTCATCAAAGCAAAGAAGCTACAAGACTCTCACTCA	AGTGTCACAAGGT 1393	ŗ	AX671108 8603 bp DNA Sequence 4 from Patent W003004523. AX671108		etazoa; Chordata; theria; Primates;	Znu,z. Regulation of human citron rho/rac-interacting kinas Patent: W0 03004523-A 4 16-JAN-2003; Bayer Aktiongesellschaft (DE) Location/Qualifiers	<ol> <li>.8603</li> <li>/organism="Homo sapiens"</li> <li>/mol_type="unassigned DNA"</li> <li>/db_xref="taxon:9606"</li> </ol>	Ouery Match 93.7%; Score 1388.2; DB 6; Best Local Similarity 99.8%; Pred No. 0; Matches 1390: Conservative 0: Mismatches 3:	GAGGGGGAATCCTTTGGATGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	CCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAACAGCACCCCTTATATGACTCAACAGCACACCCTTATATGACTCAACAAGCAACCACCCTTATAGACTCAACAAACA	いい こうけい かんしょう かんかん サイヤ あられる かんしん かいかい かいかい かんしょう かんしょう かんかん かん かんしん かんしん かんしん かんしん かんしん かんしん

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                            244 AGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCA
                                                                                                              TAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
E 1 (bases 1 to 1799)
Cloning and characterizing a novel human CRIK-SK gene
L Unpublished
E 2 (bases 1 to 1799)
S Mao,Y., Xie,Y. and Wu,Q.
Cloning sidentialism of Genetics; Fudan University,
L Submitted (02-JM-2003) Institute of Genetics, Fudan University,
220 Handan Road, Shanghai 200433, P.R. China
Location/Qualifiers
L 1.1799
L 1.1799
CACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCCCCTGCCAAGA 1320
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/note="protein kinase"
/codon strat=1
/product="citron Rho-interacting kinase short form"
/protein id="AAP43922.1"
/db xref="citron"
/db xref="citron"
/translation="MLKFKYGRNPSDAGAEPIASRASRLNLFFQGKPPFWTQQMSPRSRGILDALLVLFEECSOPALMKIGHVSNFYRKYSDTIABLQELQPSAKDFEVRSL
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HRDIKPENILVDRTGHIKLVDFGSAAKMISNKMVNAKLPIGTPDYMAPEVLTVMNGDG
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LDLIQSLLCGQKERLKFEGGCCHPFFSKIDWNNIRNSPPFYTLKSDDDTSNFDEPE
KNSWYSSSPCQLSPGOFSGEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKK
LLIKSKELQDSQDKCHKMEQEMTRLHRRVSGG"
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                                                                      CTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGACTCTCAGGACA
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/db_xref="taxon:9606"
/chromosome="12"
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Search completed: March 19, 2005, 11:54:30 Job time : 6314.06 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-791-666-3
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Sequence 26, Appl
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US-10-017-216-3
US-10-618-941-1
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US-09-964-956-10
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Sequence 1, Application US/09804471A

Batent No. US20020132322A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
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100.0%; Pred. No. 0;
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Best Local Similarity 100.
Matches 1515; Conservative
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ORGANISM: Human
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Sequence 1, Application US/10724594

Publication No. US20040091993A1

GENERAL INFORMATION:

APPLICANT: WEBSTER, Marion et al.

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

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TRIBOULEY, Catherine M. CHAWLA, Narinder K. YAO, Monique G. LU, Dyung Aina M. GREENWALD, Sara R. RAMKUMAR, Jayalaxmi GRIFFIN, Jennifer A.
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ARVIZU, Chandra S.
GURURAJAN, Rajagopal
                                                                                                                                                                                                                                                                                                                        POLICKY, Jennifer L.
                                                                                                                              BURFORD, Neil
NGUYEN, Danniel B.
TANG, Y. Tom
BAUGHN, Mariah R.
                                                                                                                                                                                                                                                                            KHAH, Farrah A.
RECIPON, Shirley A.
AZIMZAI, Yalda
                                                                                                                                                                                           HE, Ann
THORNTON, Michael
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Best Local Similarity 99.8
Matches 1512; Conservative
                                                                                                                                                                                                                                                                                                                                       DING, Li
GRETHER, Megan
                                                                                                                   KEARNEY, Liam
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SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 2066
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                661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720
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                                                                            721 GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGGATT
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CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG
                                                           GATTTTGGATCTGCCGCGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGGATT
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APPLICANT: ELLIOTT, VICKI S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: SON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; 60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-06.
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; OTHER INFORMATION: Incyte ID No. US20040023242A1 3951059CB1
US-10-311-034-33
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US-10-311-034-33
; Sequence 33, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.;
APPLICANT: INCYTE GENOMICS, INC.;
APPLICANT: BANDMAN, Olga
; APPLICANT: BANDMAN, Olga
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: AU-YOUNG, Janice

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ICCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 1308
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                                           1069 CAAAGCTTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT
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APPLICANT: Ages, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION 16052
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT APPLICATION NUMBER: 00/326,483
PRIOR PPLING DATE: 2001-10-02
PRIOR PILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/333,815
PRIOR PLING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/333,815
PRIOR PLING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/337,917
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Sequence 3, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Peyman, John A.
APPLICANT: Uu, Jingfang
APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shinger, Shlomit R.
APPLICANT: Bdinger, Shlomit R.
APPLICANT: Malyankar, Uriel M.
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Stone, David J.
Pena, Carol B. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark B.
Leach, Martin D.
Agee, Michele L.
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Ji, Weizhen
Miller, Charles E.
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Anderson, David W.
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                                     11arity 99.7%; Score 1404.2; 10 99.8%; Pred. No. 0; Conservative 0; Mismatches
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JS-10-415-011-43
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Sequence 3, Application US/10028946

Sequence 3, Application US/10028946

Sequence 3, Application No. US20020123622A1

GENERAL INFORMATION:

APPLICANT: Yu, Xuanchuan

APPLICANT: Friddle, Carl Johan

TITLE OF INVENTYON: NO. US20020123622A1e1 Human Kinases and Polynucleotides Encoding the FILE REFERENCE: LEX-0289-USA

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CURRENT APPLICATION NUMBER: US/10/028,946

PRIOR APPLICATION NUMBER: US 60/258,335

PRIOR FILING DATE: 2000-12-27

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 5877
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                                                                    GACATCAAGCCTGAGAACATTCTCGTTGACGGCACAGGACACATCAAGCTGGTGGATTTT
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; Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/329,029
PRIOR APPLICATION NUMBER: 60/329,029
PRIOR PILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-04-17
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Best Local Similarity 99.8%;
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APPLICANT: Yu, Xuanchuan
APPLICANT: Wiranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Miranda, Maricar
TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/791,666
CURRENT APPLICATION NUMBER: US/10/028,946
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2000-12-27
NUMBER: OF SEQ ID NOS: 4
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Best Local Similarity 99.8%;
Matches 1400; Conservative
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                                                                         Score 1398.2;
Pred. No. 0;
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llarity 99.8%;
Conservative
; TYPE: DNA; ORGANISM: homo sapiens US-10-028-946-3
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Best Local Similarity
Matches 1400; Conserv
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APPLICANT: Yu, Xuanchuan
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Firidale, Carl Johan
TITLE OF INVENTION: No. US20020123622Alel Human Kinases and Polymucleotides Encoding
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
PRIOR FILING DATE: 2000-12-27
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                     1387 TCTCAGGACAAGTGTCACAAGGT 1409
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PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-12-27
PRIOR PILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
TYPE: DNA
TYPE: DNA
ORGANISM: homo sapiens
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Best Local Similarity 99.8%;
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Publication No. US20040209297A1
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION WUMBER: US/10/791,666
CURRENT FILING DATE: 2004-03-02
                                                                                                                                     GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT
                                                                                                                                                                                            GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC
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                   TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA
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   GACTTGCTGTCACTTTTGAATAGATATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT
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121 ACTCAACAGCAGATGTCTCCTTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 1  133 ACTCAACAGCAGATGTCTCCTTTTCCCGAGAAGGGATATTAGATGCCTCTTTGTTCTC 1  181 TTTGAAGAATGCAGTCGCCTGCTCTGAAGAAGAATAAGATGCAGGAATTTGTTCGC 2	241 AAGTATTCCGACACTCAGCCTGCTTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA [	253 AAGTATICGACAACATTAGGTAGGTAGGAGGCICCAGCCTICGGCAAAGGGCTICGAA 31 301 GTCAGAAGTCTTGTAGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCA 36 313 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA 313 GTCAGAAGTCTTGTAGGTTGGTAACACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCA	361 ACCGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGAGGCTTTATTGGCCCAGGAGCAGAAGAGAGAG	421 GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC	481 CATTACAGTATCCCTTTCAGGACAAAATCACCTTTATCTGGTCATGAATATCAGCCT 5  493 CAATACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGAAAATCAGCTT 5  493 CAATACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGATGAAGAAAATCAGCTCT 5	541 GGAGGGACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 60 	601 CAGTITIACCTAGGTGAGCTGATTITGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 66	661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 72 	y 721 GAITTIGGAICTGCGGGAAAATGAAITCAAACAAGAIGGTGAATGCCAAACTCCCGAIT 780	y 781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGATGGATG	y 841 ACCTACGGCCTGGACTGTGACTGGTGGTGGGGGGGGGTGATTGT 900	y 901 GGGAGATCCCCCTTCGCAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 960	y 961 CAGCGGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 102:	y 1021 CAAAGCTTGTTGTGGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 108	y 1081 TICTICTCTAAAATTGACTGGAACAACATTGGTAACTCTCCCCCCCTTGGTTCCCACC 114	y 1141 CTCAAGTCCGACGATGACCTCCAATTTTGATGAACAGAAGAATTCGTGGGTTTCA 1200	y 1201 TCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG 126
	DD DD TTTTGABATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1026 TTTTTGABATTTCCAGATGACCCCAAAGTGAGGAGTGACTTTCTTGATCTGATTCAAAGC 1020	TTGTTGCGCCCCAGAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC 1086	TCAAG 1146       TCAAG 1140	TCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAATTCGTGGGTTTCATCCTCT 1206	TTCG 1266      TTCG 1260	ACTCC 1326       ACTCC 1320	CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAGAC 1386  [	1409	ko	MILITARE INFORMATION: APPLICANT: KAPELLER-LIBERMANN, Rosana APPLICANT: KAPELLER-LIBERMANN, Rosana TITLE OF INVENTION: 13245, A No. US20020160483Alel Human Myotonic Dystrophy Type Prot	017,216 Db	Qy 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.	40 da	Score 1397.8; DB 13; Length 6574; Pred. No. 0; Mismatches 7: Indels 0; Gans 0;	ATCCTTTGATGCTGGTGCTGCTGAA 60		odcienniciaiiciaticadegeennicacceiiinia 132
ACTGTGACTGGTGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	aatttccagatgaccc 	GCGGCCAGAAAGAGACACACACACACACACACACACACA	TTGACTGGAACAACAT                 TTGACTGGAACAACAT	ATGACACCTCCAATTI 	PAGCTGAGCCCCTCAGC	vaggcactggggattci                 vaggcactggggattci	AAGACTAGCTCCATGG2 	TCTCAGGACAAGTGTCACAAGGT                  TCTCAGGACAAGTGTCACAAGAT	SULT 11 -10-017-216-1 Sequence 1, Application US/10017216	N: SR-LIBERMANN, ROE N: 13245, A NO. C	FILE OF ENVENTION: Alinase and uses the FILE REFERENCE: 10147-5701 CURRENT APPLICATION UNMBER: US/10/017,21 CURRENT FILING DATE: 2001-10-23	FALOR AFFLICATION NUMBER: US 60/242,42. PRIOR FILING DATE: 2000-10-23 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.1	574 Homo sapiens	Ouery Match  Query Match Best Local Similarity 99.5%; Pre Matches 1402: Conservative 0:	TGTTGAGGTTCAATA	CCAACCGGCCTCCAG	יראפרניפפפנין ניראפ

	481 CAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 540	541 GGAGGGACTTGCTGTCACTTTTGAATAGATATGAGACCAGTTAGATAGA	601 CAGITITACCIAGCIGATITITGGCIGITACACAGCGITCATCIGAGGGIACGIG 660	661 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG 720	721 GATTTTGGATCTGCCGCAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT 780	781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGATGATGAAGAGGGATGGAAAAGGC 840	841 ACCTACGGCCTGGACTGTGACTGGTCGGCGTGGTGTTGCTATGAGATGATTAT 900	901 GGGAGATTCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC 960	961 CAGCGGTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGAICTGAIT 1020	1021 CAAAGCTTGTTGTGCGGCCAGAAAGAGACACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1080	1081 TTCTTCTCTAAATTGACTGGAACAATCGTAACTCTCCCCCCTTCGTTCCTCCCCC 1140	1141 CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAATTCGTGGGTTTCA 1200	1201 TCCTCTCCGTGCCGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGG 1260	1261	1321 GACTCCCTGCCAAGACTAGCTCCATGGAAAGAAACTTCTCATCAAAGCAAAGGCTA 1380	1381 CAAGACTCTCAGGACAAGTCTCACAAGGT 1409 	RESULT 13 US-10-757-262-51 ; Sequence 51, Application US/10757262 ; Publication No. US20040197825A1 ; GENERAL INFORMATION:
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## APPLICANT: Karicheti, Venkateswarlu
### APPLICANT: Silose-Santisgo, Immaculada
### APPLICANT: Silose-Santisg
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92.3%;
Best Local Similarity 99.5%;
Matches 1402; Conservative C
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; LOCATION: (19)...(6180)
US-10-757-262-51
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ORGANISM: Homo sapiens
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Sequence 11, Application US/10325430

Publication No. US20030153525A1

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Rosenfeld, Unlie Beth
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
TITLE OF INVENTION: 32838 338 and 52908
FILE REFERENCE: MPIOL 29441RNM
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/341,953
PRIOR APPLICATION NUMBER: US 60/341,953
PRIOR APPLICATION UNBER: US 60/341,953
NUMBER OF SEQ ID NOS: 21

SOFTWARE FEASES for Windows Version 4.0
SEQ ID NO 11
LENGTH: 6162
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                                                             Sequence 3, Application US/10017216
Publication VO US20020160483A1
GENERAL INFORMATION
TITLE OF INVENTION: 13345, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prof
TITLE OF INVENTION: Kinase and Uses Therefor
TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-57U1
CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO
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Matches 1396; Conservative
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ORGANISM: Homo sapiens
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US-10-017-216-3
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                                               DB 16;
                                              Score 1391.8;
Pred. No. 0;
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Best Local Similarity 99.5%;
Matches 1396; Conservative
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; FEATURE:
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Search completed: March 19, 2005, 18:10:54 Job time: 833.8 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-422-699A-10	US-08-422-706B-10	US-09-442-100-7	US-08-939-106-7	US-09-442-102-7	US-09-509-902A-6	US-09-509-902A-15	US-09-233-857-2	US-08-860-150-6	US-09-338-132-6	US-08-878-989-11	US-09-272-796-11	US-09-442-100-5	US-08-939-106-5	US-09-442-102-5	US-09-248-796A-4400	US-09-588-256-1	US-09-442-100-1
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156.4	156.4	125.8	125.8	125.8	125.4	125.4	125.4	121	121	114.6	114.6	113	113	113	110.4	108	104.6
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Sequence 1, Application US/09804471A

Sequence 1. Application US/09804471A

Patent No. 6479269

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLO01164

CURRENT APPLICATION NUMBER: US/09/804,471A

CURRENT FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FRALEGO FOR Windows Version 4.0

SEQ ID NO 1
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ORGANISM: Human
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420 Qy 1501 GCCGCTGATCCGTA 1515 480 Db 1501 GCCGCTGATCCGTA 1515 480	Sequence   Application US/10238709   Application   Acid Moderates   Ac	840 Query Match 100.0%; Score 1515; DB 4; Length 1515; Best Local Similarity 100.0%; Pred. No. 0; Matches 1515; Conservative 0; Mismatches 0; Indels 0; Gap.	900 OY 1 GGGGAGATGTTGAAGTTCAAATATGAGGGGGGAATCCTTTGGATGCTGGTGCTGCTGAA 	960 61 CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGCTTCTTCCAGGGGAAACCACCTTTATG	1020  OY 121 ACTCAACAGATGTCTCCTCTTTCCCGAGAAGGATATTAGATGCCTCTTTGTTCTC	1080  Qy 181 TITGAAGAATGCAGCTCGCTCTGATGAAGATTAAGCACGTGAGCAACTTGTCCGG	1140	1200 QY 301 GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAGAAAAACA	260 OY 361 ACCGGGGACATCTATGCTATGAAGTGATGAAGAAGAGCTTTATTGGCCCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	Qy   421 GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCCCGTGGATCCCC	1380 Qy 481 CAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCTT	1440	1500 Qy 601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG
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0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/258,335
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Friddle, Carl Johan
TITLE OF INVENTION: 0. 6734009el Human Kinases and Polynucleotides |
PILE REPERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
                        CATCGAGACATCAAGCCTGAGAACATTCT
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Patent No. 6734009
GENERAL INFORMATION:
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Sequence 1, Application US/09916204

Sequence 1, Application US/09916204

Batent No. 6638745

GRNERAL INFORMATION:

GRNERAL INFORMATION:

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THERED PROTEINS, AND USES TITLE OF INVENTION: THERED PROTEINS, AND USES TITLE OF INVENTION: NUMBER: US/09/916,204

CURRENT APPLICATION NUMBER: US/09/916,204

CURRENT FILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1.13
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ORGANISM: Human
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 965; Conserv
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US-09-774-528-419
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US-10-282-048-1
US-10-282-048-1
; Sequence 1, Application US/10282048
; Patent No. 669248
; GENERAL INFORMATION:
; APPLICANT: WEI, MING-Hui et al.
; TITLE OF INVENTION: THERED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: THEREDOF
; TITLE OF INVENTION: THEREDOF
; TITLE OF INVENTION: THEREDOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 1
; SEQ ID NO 1
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                                                                                      CCATTGCCAGCCGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATG 167
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                                                                         CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG
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Mismatches
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Conservative
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TYPE: DNA
ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FPLING DATE: 2000-10-20

PRIOR PLLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                           GGGGAGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGCTGCTGAA
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  Length 1133;
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Score 760.8; DB 4;
Pred. No. 5.3e-244;
0; Mismatches 2;
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Query Match 50.2%;
Best Local Similarity 99.7%;
Matches 762; Conservative
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1166 ATTTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCCCT 1225
                      1858 TGTCTGAAAATGCTAAGGATCTTATTCGAAGGCTCATTTGTAGCAGAAAAACATCGACTTG 1917
                                                                                                                                                                                        1978 ATATTCGGAACTGTGAAGCACCTTATATTCCAGAAGTTAGTAGCCCAACAGATACATCGA 2037
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                                                                                                            -----GAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTCTTAAAATTGACTGGAACA
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APPLICANT: Brown David E.

APPLICANT: APPLICANT: Alarley, Helen J.

APPLICANT: Harley, Helen G.

APPLICANT: Harley, Helen G.

APPLICANT: Harley, Helen G.

APPLICANT: Johnson, Keith J.

TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF NUMBER OF SEQUENCE: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLING DATE: 20-FED-----
FILING DATE: 20-FED-----
PRIOR BALICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
APPLICATION 19-FEB-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FBE-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08422699A Patent No. 5955265
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
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CITY: Lexington
STATE: Massachu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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US-08-422-699A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 234.6; DB 4; Length 2423;
Pred. No. 2.9e-67;
0; Mismatches 519; Indels 15;
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.5%;
52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 52.5
Matches 591, Conservative
                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-2640
                                                                                                                                                                                                                                                                     LENGTH: 2423
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Gaps
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                                                                                                                                                                                                                                                                         APPLICANT: Brook, J. David
APPLICANT: Housman, David B.
APPLICANT: Shaw, Duncan J.
APPLICANT: Shaw, Duncan J.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
COUNTRY: US
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Pred. No. 3.3e-64;
0; Mismatches 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.30
                                                                  1145 AGTCCGACGATGACACCTCCAATTTTGA 1172
                                                                                                           1203 AAGGTGCCACCGACACATGCAACTTCGA 1230
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-5540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FGB-1993
FRICR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
                                                                                                                                                                                                             Sequence 12, Application US/08422706B Patent No. 5977333 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                            CTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTT 319
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                                                                                                                                                                                                                                                            CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACATAG
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                                                                                                                                                                                                                    15;
                                                                                                                                                                             Length 2726;
                                                                                                                                                                                                                    0; Mismatches 439; Indels
                                                                                                                                                                         Score 225.6; DB 2;
Pred. No. 3.3e-64;
                                                                                                                                                                             Query Match
Best Local Similarity 54.0%;
Matches 534; Conservative
                                                 LENGTH: 2726 base pairs;
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
1 TOPOLOGY: linear
US-08-422-699A-12
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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APPLICANT: Brook, J. David
APPLICANT: Brook, J. David
APPLICANT: Alaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massach....
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Pred. No. 6e-62;
0; Mismatches 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
FILING DATE: 09-FEB-1993
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTOWNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INPORMATION:
TELEPAX: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
FRIOR PRELICATION DATA:
APPLICATION NUMBER: US 07/839,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
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Best Local Similarity 54.5%;
Matches 511; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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; LOCATION:
US-08-422-699A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                          CTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAG 259
                                                                                                                                                        CTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTT 319
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                                                                                                    243 ccaaacrigacccagaacaagracgragaccaacrigacagragagacccarcard
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US-08-422-699A-8
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STREET: Two Militia Drive Smith & Reynolds, P.C. STREET: Two Militia Drive STATE.
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOWNUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB9202485.0 FILING DATE: 06-FEB-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.5%;
Matches 511; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2511 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2511 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..1746
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LOCATION:
US-08-422-706B-8
                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATCCTTTCTTCTCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTT 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCCCGAGTGTGACTGGTGGGCGCTGGTATTCGCCTATGAATGTTCTATGGCAG 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907 ICCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAAIAACATTAIGAATTTCCAGCGG 966
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                                                   103 GTGATCGGACGCGGGCCGTTCAGCGAGGTAGCGGTAGTGAAGATGAAGCAGACGGCCCAG 162
                                                                                                                     370 AICTAIGCIAIGAAAGIGAIGAAGAAGAAGAGGCITIAIIGGCCCAGGAGCAGGIIITCAIII 429
                                                                                                                                                                                   GTGTATGCCATGAAGATCATGAACAAGTGGGACATGCTGAAGAGGGGGGAGGTGTCGTGC 222
                                                                                                                                                                                                                                                    TTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCCGTGGATCCCCCAATTACAG 489
                                                                                                                                                                                                                                                                                                                  Trecerdaddaddadderregreangaargddaaccedddagarcacddagcrecac 282
                                                                                                                                                                                                                                                                                                                                                                                    490 TATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGAC 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGAGAC 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGCGGAGATTGTCATGGCCATAGACTCGGTGCACCGGCTTGGCTACGTGCACAGGGAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTTGGA 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGCCTCAAGCTGCGGGCAGATGGAACGGTGCGGTCGCTGGTGGCCTGTGGGCACAACAA 582
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                                                                               250 GACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGGTCAGAAGT 309
                                                                                                                                                                 310 CTTGTAGGTTGTGGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGGGAC 369
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                                                                                                                      43 GCCATCGTGGTGAGGCTTAAGGAGGTCCGACTGCAGAGGGGACGACTTCGAGATTCTGAAG 102
                                                                                                                                                                                                     TITGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTACAG 489
                                                                                                                                                                                                                                                                                                                                                                       163 grerareccareaagarcareaacaacreesacarecreaagaeseseseseseserere
                                        15;
    Length 2511;
                                        Indels
Score 218.8; DB 2;
Pred. No. 6e-62;
0; Mismatches 412;
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Sequence 8, Application US/08422706B

Patent No. 597333

GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Housman, David APPLICANT: Harley, Helen G.
APPLICANT: Harley, Helen G.
TITLE OF INVENTION: DYA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

RESULT 12 US-08-422-706B-8

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1043 GCTGACACTGCTGAGCAAGTTTGGGGAGCGGATTCCGGCCGAGATGGCGCGCTTCTACCT 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                923 CCGTGAGGAGAGGGACGTGTTGGTGAATGGGGACCGGCGGTGGATCACGCAGCTGCACTT 982
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                                                                                                                                US 08/019,940
         APPLICATION NUMBER: US/08/484,044
                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: PAUL, THOMBER: 32,714
REFERENCE/DOCKET NUMBER: D-54/
TELECPHONICATION INFORMATION:
TELEPHONE: 713/651-525
TELEPHONE: 713/651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3182 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 762829
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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; MOLECULE TYPE: DNA
US-08-484-044-11
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APPLICANT: Caskey, C. T.
APPLICANT: Fr, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Friedman, David L.
APPLICANT: Prisuti, Antonio
APPLICANT: Penwick, Raymond G.
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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STATE: Texas
COUTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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1301 McKinney, Suite 5100
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; Patent No. 5552282
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US-08-484-044-11
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APPLICANT: WEBSTER, Marion et al
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION:
TITLE OF INVENTION:
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION:
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                                                                            969 TTTGAAATTTCCAGATGACCCCAAAGTGAGCAGT----GACTTTCTTGATCTGATTCAAAG 1025
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1403 GCCCTTCTACGCGGATTCCACGGCGGAGACCTATGGCAAGATCGTCCACTACAAGGAGCA 1462
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14.3%; Score 216.2; DB 4; Length 174493;
Best Local Similarity 96.5%; Pred. No. 8.7e-60;
Matches 221; Conservative 0; Mismatches 8; Indels 0;
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i LOCATION: (1)...(174493)
CTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3
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Patent No. 668018
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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ORGANISM: Human
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ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF

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171282 irrirrcrcraccinaggicifgirgifgiteggarcregacitececteceaagacraectar 171341
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Pred. No. 8.7e-60;
0; Mismatches 8;
FILE REFERENCE: CL001164DIV
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PREISEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 174493
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time: 271.502 secs
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| LOCATION: (1)...(174493)
| OTHER INFORMATION: n = A,T,C or
US-10-238-709-3
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96.5%;
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Best Local Similarity 96.5
Matches 221; Conservative
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ORGANISM: Human
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Query Match
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BG908196 2082-86 M
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BG944539 ax511611.x
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                                                           March 19, 2005, 07:45:41; Search time 4592.53 Seconds (without alignments) 12556.766 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                         nucleic search, using sw model
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BG808196
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CK841805 UI-R-BJOP BB827314 BB827314 BYO18641 BYO18641 CG655761 OCST426725 BF944809 PM3-NN117 CB744826 UI-M-GVO-CF744580 UI-M-GVO-CF744580 UI-M-GVO-BU475240 603844069 BU467540 603844069 BU467540 603844069 BU467540 603844069 BU467540 603844069 BU67540 BYC02044 BCC24150 MUS MUSCUL BYC02044 BYC02044 BCC24150 MUS MUSCUL BYC02041 BYC02044 BCC3410916 STrPu691 BYC01399 BYC01399 BR823725 BB823725 BCC38993 HOMO SAD1	ENTS	BP146990 BP146990 full-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVEM10025B09 5', mRNA sequence. BP146990.1 GI:40396461 BP146990.1 GI:4039641 BP146990.1 GI:40396941 BP146990.1 GI:403969941 BP146990.1 GI:40396941 BP146990.1 GI:403969494994994949694949496949494969494949694949496949494949494949494949494949694949494969649494969694949496969494949696949494969699494949696994949496994969699494949696994949496969949494949494949494949494949494949494949	
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		RESULT 1 BP146990 LOCUS DEFINITION ACCESSION VEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT COMMENT FEATURES SOURCE SOURCE	

Length 698;

39.8%; Score 602.6; DB 5; 91.4%; Pred. No. 2.9e-172;

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CR746615 CR746615 NIH MGC 72 Homo sapiens cDNA clone IMAGp998D0712279 ; IMAGE:5557590 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 crcescreaachachccccrrreresscrrrrcgrachachachachcresscrrres 420
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                   /clone="IMAGE:5557590"
/tissue type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NHH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT Average insert size 2 kb. Library constructed by Life rechnologies."
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLANL.gov d column: 07
High quality sequence stop: 510.
Location/Qualifiers
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                                                                                                                                                             sapiens"
                                                                                                                                                         /organism="Homo sapier
/mol_type="mRNA"
/db_xref="taxon:9606"
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DEFINITION
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_6699306 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557590
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(Dases 1 to 1085)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                 CAGGAGCAGGTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCG
                                                                                                                                       TGGATCCCCCAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Prestation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
           ö
           60; Indels
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         638; Conservative
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600 bp mRNA linear EST 20-DEC-2001 retina lambda ZAP II Library Mus musculus CDNA,
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Mu, Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W., White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H. Gene expression in the developing mouse retina by EST sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 AAGTATTCCGACACCATAGCCGAGTTGCGGGAGCTGCAGCCGTCGGCGAGAGACTTCGAA 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 CCCATTGCCAGTCGGGCCTCCAGGCTAAATCTCTTCTTCCTGGGGAAACCGCCCCTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 ACTCAACAGCAGATGTCTGCTCTTTCCCGGGAAGGGATGCTAGACGCCCTCTTCGCTCTC
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/db_xref="taxon:10090"
/tismue_type="neural retina"
/dev_stage="embronic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
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Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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86.6%; Pred. No. 1.9e-126;
ive 0; Mismatches 77;
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                                                                                                                                2082-86 Mouse E14.5
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Best Local Similarity 86.6
Matches 499; Conservative
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      485 CATGGAAA 492
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215 CAACATTCGTAACTCTCCCCCCTTCGTTCCACCTCAAGTCTGAACATGACACCTC 304
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/clone="taxon:9606"

/clone="thAc699800712279; IMAGB:5557590"

/tissue_type="melanotic melanoma"

/tissue_type="melanotic melanoma"

/tissue_type="melanotic melanoma"

/clone_lib="NIH MGC_72"

/clone_lib="NIH MGC_72"

/note="Organ: Rkin; Vector: pCMV-SPORT6; Site_1: Not1;

/average_insert_size_2 kb. Library constructed by Life

Technologies.
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1 (bases 1 to 492)
Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., 1
Betrs, M., Radelof, U. and Schneider, D.
I.M. A.G.E. cDNA Clone Collection
Unpublished (2004)
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/organism="Homo sapiens"
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BG944539 427 bp mRNA linear EST 15-JAN-2003 ax51f11.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library) Homo sapiens cDNA clone ax51f11 random, mRNA sequence.
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Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9817, National Institutes of Health, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=10rgan: blood, Vector: Lambda ZAP II, Site 1: ECORI, Site 2: ECORI, 65,000 proliferating erythroid cells from the buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3)
                                               240
                                                                                                                         298
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                                                                                                                                                                                                                                                                                              299 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 358
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1 (bases I to 427)

Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.

Gene expression in proliferating human erythroid cells

Genomics 59 (2), 168-177 (1999)
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                                                                                           239 TITGAAGAATGAAGTCAGCTGCTCTGAIGAAGAITAAGCACGTGAGCAACTITGTGCGG
                                                                                                                                                                                                                                                                                                                                                                                GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCA
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                                                                                                                                                                                                                AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA
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Intramural Sequencing Center (NISC).
Plate: 51 row: f column: 11
Seq primer: -21M13 forward primer (ABI).
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/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Monomuclear Cells"
/dev stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="ax51f11"
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Fax: 301 435 5148
Email: jm7f@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR746792 NCI CGAP Brn64 Homo sapiens CDNA clone IMAGP998E239412 ; https://dx.es.et.419886 5', mRNA sequence.
                                                                                      540
                                                                                                                                  ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCT 238
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445 GTTTCATTTTTCGAGGAGGAGGAACATATTATCTCGGAGCACGAGTCCTTGGATCCCC 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mkNa" orpromotion of the property o
                                                                              CAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAGp998E239412.
RZPDILB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTATTCCGACACCATAGCTGAGTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTTGTGGTCAC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGAAGTCTTGTAGGTTGTGGTCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITGCTGAAGTGCAGGTGGTAAGAGAAAGCAACCGGGGACATCTATGCTATGAAAGTG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTTCATTTTTTGAGGAAGAGGCGGAAC 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ATGAAGAAGGCTTTATTGGCCCAAGGAGCAGGTTTCATTTTTTGAGGAAGAGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ATATTATCTCGAAGTACAAGCCCGTGGATCCCTCAATTACAGTATGCCTTTCAGGACAAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 AATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGACTTGCTGTCACTTTTGAAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                     Clontech's Capfinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and clond into EcoRi digested Lambda Zap II vector and Strategene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the CDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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TR:088937 088937 RHO/RAC-INTERACTING CITRON KINASE SHORT ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTCAGCCTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGAGAAGGGATATTAGATGCCCTCTTTGTTCTTTTGAAGAATGCAGTCAGCCTGCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATTATCTCGAAGCACAAGCCCGTGGATCCCCCCAATTACAGTATGCCTTTCAGGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGGGGCACTTGCTGTCACTTTTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Endocrine Pancreas Consortium
ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                  Length 427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                           Score 423.8; DB 4;
Pred. No. 1.2e-117;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.0%;
Best Local Similarity 99.5%;
Matches 425; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATATG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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BQ417810
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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                                                                                                                                                                                                                                                                                                       DRIGIN
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/dev_stage="nc. 14.5"
/lab_host="E. coli-DH12S (GIBCO)"
/clool lib="Kasestner ngn3 wt"
/note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
/note="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site_1:
Not I; Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and Sall linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-Sall sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/-. The wt library is in
pSPORT1, T7 promoter is 5'."
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                                                              Tel: 617-495-1812
Fax: 617-495-812
Fax: 617-495-825.
Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: Dr. Marie Scearce
(mscearce@mail.med.upenn.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 367.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 AAGTATTCCGACACCCATAGCCGAGTTGCGGGAGCTGCAGCCGTCGGCGAGAGACTTCGAA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge.
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 CCCATTGCCAGTCGGGCCTCCAGGTAAATCTCTTCCAGGGGAAACCGCCCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCATTGCCAACCGGGCCTCAGGCTGAATCTGTTCCAGGGGAAACCACCTTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACTCAACAGCAGATGTCTCCCTTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 ACTCAACAGCAGATGTCTGCTCTTTCCCGGGAAGGGATGCTAGACGCCCTCTTCGCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 TTTGAAGAGTGCAGCCAACCCGCCCTGATGAAGATGAAGCACGTGAGCAGCTTTGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCA
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Pred. No. 2.4e-114;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                            1. .617
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="129/Sv x CD1"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.3%;
Best Local Similarity 86.1%;
Matches 457; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387
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us-10-724-594-1.rst

RESULT 8 CN682405 LOCUS

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Mus musculus
                                           Similarity
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                             Query Match
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CN678533
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
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Sharov, A.B., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., Vancov, A.B., Piao, Y., Martin, P.R., Stagg, C.A., Bassey, U.C., VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., Tanaka, T., G., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Kulotz, E., Kelsoe, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.
Transcriptome analysis of mouse stem cells and early embryos Contect: Dawood B. Dudekula
Laboratory of Genetics
            CN682405 Halbp mRNA linear EST 17-MAY-2004 CO164804-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, low density) cDNA library (Long) Mus musculus cDNA clone NIA:E0164B04 IMAGE:30782511 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0164 row: B column: 04
Seg primer: M13 Reverse
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/db_xref="niaEST:E0164804-5"
/db_xref="taxon:10090"
/clone="NIA:E0164B04 IMAGE:30782511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 481
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                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
                                                                      CN682405
CN682405.1 GI:47448856
                                                                                                                                 Mus musculus
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KEYWORDS
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AUTHORS
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FEATURES

COMMENT

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P. Urso, M., Kelso, J., Hide, W. and Ko, M.S.

Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GATCCAGTTTTACCTTGCTGAGCTGATTTTGGCTGTCCACAGGGTGCACCAGATGGGATA 360
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ACAGGTTTCATTTTTCGAGGAGAGAGGACATGTATTATCTCGGAGCACGAGTCCTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CCCCCAGTTACAGTACGCCTTTCAGGACAAAAAAAAAACCTTTACCTGGTCATGGAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GCCTGGAGGGGATTTGCTGTCGCTTCTGAACAGATACGAGGACCAATTAGATGAGAGCAT
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                                                                                                                                                                                                                                                                           297 CGAAGTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAA
                                                                                                                                                                                                                                                                                                                                1 CGAAGTTCGAAGCCTTGTGGGGCTGTGGTCACTTCGCTGAAGTGCAGGTGCAGGTTAGAGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597 GATACAGITITACCIAGCIGAGCIGATITIGGCIGITCACAGCGITCAICIGAIGGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 CGTGCATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 TGTGCATCGAGACATCAAGCCCGAGAACATCCTCATCGACCGGACGGGACACATCAAGCT
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
average insert size is about 2.8 kb. The library constructed by Yulan Piao."
                                                                                                                                                                                                            .;
m
                                                                                                                                  Length 481;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                     55;
                                                                                                                              Score 380; DB 7; I
Pred. No. 3.2e-104;
0; Mismatches 55;
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                                                                                                                                         25.1%;
88.0%;
                                                                                                                                                                                                     Matches 426; Conservative
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University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID= 1797673
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                               EST 12-DEC-2000
301 GATCCAGTTTTACCTTGCTGAGCTGATTTTGGCTGTCCACAGCGTGCACCAGATGGGATA 360
                                                   716
                                                                  361 TGTGCATCGAGACATCAAGCCCGAGAACATCCTCATCGACCGGACGAGCACATCAACGT 420
                                                                                                                                   421 GGTGGATTTTGGATCAGCCGCTAAGATTCAAATAA---GGTGGATGCCAAACTCCC 477
                                                                                                                717 GGTGGATTTTGGATCTGCCGCGAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCC 776
                                                                                                                                                                                                                                                                                              BFS62826
UI-R-BJOp-aip-b-06-0-UI.rl UI-R-BJOp Rattus norvegicus CDNA clone
UI-R-BJOp-aip-b-06-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                 657 CGTGCATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.2%; Score 351.4; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
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                                                                                                                                                          /db_xref="niaEST:E0112C12-5"
/db_xref="taxon:10090"
/clone="NIA:E0112C12 IMAGE:30777539"
                                                                                                                                                                                                                             /tissue type="Embryonic Stem Cell"
/cell line="129.3 ES cells"
/lab_host="DH108"
                                                                                                              organism="Mus musculus"
Email: cdna@lgsun.grc.nia.nih.gov
             Plate: E0112 row: C column: 12
Seq primer: M13 Reverse
High quality sequence stop: 479
POLYR=No.
                                                                                                                              /mol_type="mRNA"
/strain="129Sv/EvTac"
                                                                                Location/Qualifiers
                                                                                                                                                                                                               'sex="Male"
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Best Local Similarity 88.0<sup>†</sup>
Matches 424; Conservative
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Best Local Simil
Matches 469;
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DEFINITION
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AUTHORS
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603280370F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5310496 5',
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1 (bases 1 to 821)
1 Marhado http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                           ACTCAACAGCAGATGTCTGCTCTTTCCCGGGAAGGGGTGTTAGATGCCCTCTTTGTTCTC
                                                                                                                                                                                                                                                 AAGTATTCTGACACGATAGCCGAGTTACGGGAGCTCCCAGCCGTCGGTGAGGGACTTCGAA
                                                                          CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATG
                                                                                                                                                                     ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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cDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNI
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information of
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1786 row: 1 column: 17
High quality sequence stop: 648.
Location/Qualifiers
                 ö
                                              GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGG
 Pred. No. 1.8e-95;
0; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
/db.xref="taxon:10090"
/clone="IMAGS:5310496"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTC 457
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BI654262
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               391; Conservative
Similarity
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/clone_lib="NCI_CGAP_Mam4"

/note="Organ: mammary; vector: pCMV-SPORT6; Site_l: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Öligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lochar Hennighausen/Priscilla Furth,

NIH Reference for transgenic model: Li et al., Cell Growth

and Differentiation 7, 3-11 (1996)."
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Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, B.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Rey, B.W. Jr., Kipp, P., Kohlhauff, B., Man, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 CCCATTGCCAGTCGGGCCTCCAGGTAAATCTCTTCCAGGGGAAACCGCCCCTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 AGGTTCGAAGCCTTGTGGGCTGTGGTCACTTCGCTGAAGTGCAGGTGCTTACGAGGAAG
                                                                                                                                                                                                                                                                                                                                                              GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCTTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 A-GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGG-TAAGAGAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 GCGACCGGGGACGTCTATGCCATGAAAATCATGACAGAAGAAGGCTTTGCTGGCCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          521 ACAGGTTTCATTTTTCGAGGAGGAGGAACCATATTATCTCGGAGCACGAGTCCTTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 TCCCCCAATTACAGTATGCCTTTCAGGA-CAAAAATCACCTTTATCTGGTCATGG--AAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAACCGGGGACATCTATGCTATGAAAGTGATGA-AGAAGAAGGCTTTATTGGCCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 GCAGGITTCATTTTTGAGGAAGAGCGGAA-CATATTATCTCGAAGCACAAGCCCGTGGA
                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                  Length 821;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                               Score 344.2; DB 4;
Pred. No. 3.5e-93;
0; Mismatches 78;
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Mus musculus
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ilarity 84.5%;
Conservative
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JOURNAL

COMMENT

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CG501399 449 bp mRNA linear GSS 01-0CT-2003 OST45249 Mus musculus cDNA clone OST45249, mRNA sequence. CG501399 CG501399.1 GI:37275067 GSS
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 449)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol type="mixed original orig
                             Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiAM9412 row: e column: 23
High quality sequence stop: 423.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
       Contact: Robert Strausberg, Ph.D.
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1184 AGAATTCGTGGGTTTCATCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAG 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1244 AACTGCCGTTTGTGGGGTTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGT 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTTGTGTGGGGTCTGGACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCA 1363
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Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Yab, Q., Person, C. and Sands, A.T.
Whyl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 423)

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/cell type="embryonic stem cell"
/clone_lib="Mus musculus 1295v/Ev"
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Pred. No. 1.1e-88;
0; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .450 /organism="Mus musculus"
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/strain="129Sv/Ev"
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Best Local Similarity 90.0%;
Matches 352; Conservative
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                                                                                                                                                                                                                                      Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9,392(6676):608-11)
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Whil kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACAGCCGGCCTACGTCCTTGCTCCAGGATCCTCCCAGTCATATATGCCGAGGGATCTG 365
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                        Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 327; DB 9; Length 449;
Pred. No. 5.1e-88;
0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
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/mol_type="mRNA"
/strain="129Sv/Ev"
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/clone="OST45249"
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Best Local Similarity 91.8%;
Matches 345; Conservative
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Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fright, J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Rey, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markeslch, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
Whkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                               4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag genered by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1238 GTGAAGAACTGCCGTTTGTGGGGTTTTTCGTACAGGCAAGGCACTGGGGATTCTTGGTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GCGAAGAGCTGCCGTTTGTGGGATTTTCGTACAGCAGAGGCACTGGGGATATTTGGTAGAT
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/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.0%; Score 318.2; DB 9; 92.0%; Pred. No. 2.6e-85; ive 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .512
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol type="mRNA"
/strain="1295v/Ev"
/db_xref="taxon:10090"
/clone="0ST417039"
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Matches 346; Conservative
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Copyright (c) 1993 - 2005 Compugen Ltd.
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March 19, 2005, 06:24:41; Search time 767.108 Seconds (without alignments) 11691.196 Million cell updates/sec Run on:

US-10-724-594-1 1515

Title: Perfect score:

1 ggggagatgttgaagttcaa......tctgagccgcctgatccgta 1515 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4390206 segs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters:

8780412

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aca61394 CDNA enco	AadS9938 Human kin Ado40591 Human kin	Aad26454 Human kin	Abz68726 Nucleotid	Abz68725 Nucleotid	Aad38864 Human kin	Ada05643 Human NOV	Abg78871 Human kin	Aal55217 Human CRI	Abg78870 Human kin	Aal55214 Human CRI	Aal55215 Human CRI	Aad39191 Human MDP	Adf60992 Pain asso	Adq89099 Human uro		Adf60993 ORF of pa	Adj96544 Human cit	Aas06701 Polynucle
SUMMARIES	<u> </u>	ACA61394	AAD59938 AD040591	AAD26454	ABZ68726	ABZ68725	AAD38864	ADA05643	ABQ78871	AAL55217	ABQ78870	AAL55214	AAL55215	AAD39191	ADF60992	ADQ89099	ADN62808	ADF60993	ADJ96544	AAS06701
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## ALIGNMENTS

Human; 88; gene; gene therapy; kinase; antisense. 1..6 7..1500 /\*tag= b /product= "Kinase" 1501..1515 /\*tag= c Location/Qualifiers cDNA encoding novel human kinase. ACA61394 standard; cDNA; 1515 BP. 11-AUG-2003 (first entry) US2003022340-A1. Homo sapiens. ACA61394; Key 5'UTR 3' UTR RESULT 1 ACA61394 SOS XTTTTTTTTTX

30-JAN-2003.

11-SEP-2002; 2002US-00238709.

(APPL-) APPLERA CORP.

13-MAR-2001; 2001US-00804471.

Webster M, Yan C, Di Francesco V, Beasley EM;

WPI; 2003-438978/41. P-PSDB; ABU10126.

New human kinase peptides useful as models or targets for the development of therapeutic agents that modulate kinase activity, for eliciting immune response, and in identifying compounds that modulate kinase activity or expression.

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Human, kinase protein, diagnostic, therapeutic, immune response, pharmacogenomic, tissue typing, gene therapy; chromosome 12; transgenic;
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                            The invention relates to a novel isolated human kinase. The kinase peptides and nucleic acids are useful as models for the development of human therapeutic targets, in the identification of therapeutic proteins, and serve as targets for the development of human therapeutic gents that modulate kinase activity in cells and tissues that express the kinase.

The proteins can be used to raise or to elicit another immune response, as a reagent in assays designed to determine the levels of the protein in blological fluids, as markers for tissue in which the corresponding protein is preferentially expressed, in the identification of modulators of the peptides and in pharmacogenomic analysis. The nucleic acids are useful as hybridisation probes, in constructing vectors, host cells or transgenic animals expressing all or a part of the nucleic acid, for monitoring the effectiveness of modulating compounds on the expression or activity of the transporter gene in clinical trials or in treatment regimen, in gene therapy and as antisense constructs to control transporter gene expression in cells, tissue and organisms. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human kinase proteins, useful as models for developing human therapeutic targets, or for treating a disorder associated with an absence of, inappropriate or unwanted expression of the protein, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a kinase polypeptide and its encoding polynucleotide. The polypeptide and polynucleotide of the invention are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. The invention is also useful for biological assays related to kinase, in drug screening assays, for treating disorders characterized by an absence of inappropriate and unwanted expression of the protein. The present sequence is human kinase cDNA. The human kinase gene is located on chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human kinase proteins and nucleic acids, useful for developing human therapeutic targets, identifying therapeutic proteins eserve as targets for the development of human therapeutic agents that modulate kinase activity.
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kinase related disorder, human, chromosome 12; gene, ss.
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Pred. No. 0;
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Best Local Similarity 100.0%;
Matches 1515; Conservative 0
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(first entry) 26-MAR-2002 AAD26454; X4X5X4X6X6X6X6X6X6X6X6X6X6X6X6X

Human kinase PKIN-7 cDNA.

Human; kinase; PKIN-7; cancer; leukaemia; adenocarcinoma; osteoarthritis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mallitus; osteoporosis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardiovascular disease, hypertension; vasculitis; myocarditis; obesity; fatty liver; Niemann-Pick's disease; gene therapy; ss.

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187

240

180

Homo sapiens

/\*tag= a /product= "Human PKIN-7 protein" Location/Qualifiers 14. .1507

20-DEC-2001

WO200196547-A2

14-JUN-2001; 2001WO-US019444.

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The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, Hodgkin's disease) immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, ansemia, allergies, adult respiratory distress syndrome, atherosclerosis, activities, crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, graves' disease, osteoarthritis, osteoporosis, pancreatitis, Crohn's disease, diabetes chemmatodia rathritis, Sjogram's syndrome, uveitis, ulcerative colitis, contentation, slogram's syndrome, uveitis, ulcerative colitis, contentation, viral, protozoal and helminthic infections) contentating's syndrome, hypothyroidism, cerebral palay, astarateds; cardio cyascular disease (arteriovenous fistula, hypertension, vasculitis, congestive heart failure, angina pectoris, myocarditis, aneurysms, congestive heart failure, angina pectoris, myocarditis, congestive heart failure, angina pectoris, myocarditis, consensing toxicity of a ischaemic heart disease, chronic bronchitis, the present sequence is human provent and a in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.
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                                                                                                                                                                                                                           Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Rearney L, Burford N, Nguyen DB, Tang YT; Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
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15-JUN-2000; 2000US-021367P.
23-JUN-2000; 2000US-0213467P.
30-JUN-2000; 2000US-0215651P.
07-JUL-2000; 2000US-0216605P.
13-JUL-2000; 2000US-0218972P.
25-AUG-2000; 2000US-0218972P.
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Best Local Similarity 99.8%;
Matches 1512; Conservative
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P-PSDB; AAE16261.
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The present sequence encodes a human citron rho/rac-interacting kinase-short kinase polypeptide. The polymucleotide and polypeptide of the invention are useful in preventing, ameliorating, or treating diseases associated with the polypeptide dysfunction. The expression vector or the reagent is useful in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase-short kinase in a disease, such as obesity or chronic obstructive pulmonary disease. These may also be used for treating obesity/ overweight-associated comorbidities, such as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced
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                                                                Length 1765
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                                T; 0 U; 0 Other;
                                                                                             2; Indels
                                                                DB 10;
                                                           Score 1505.8;
Pred. No. 0;
0; Mismatches
                               Sequence 1765 BP; 428 A; 430 C; 444 G; 463
                                                            Query Match
Best Local Similarity 99.9%;
Matches 1507; Conservative
and depression
fertility,
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PR 25-APR-2002; 2002US-0375015P.

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Zhu Z;
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WPI; 2003-221595/21.

DR P-PSDB; ABP97681.

XX
WPI 2003-221595/21.

DR P-PSDB; ABP97681.

XX
New human citron rho/rac-interacting kinase-short kinase polypeptide and polymocleotide for preventing or treating diseases associated with the polymocleotide for preventing or treating diseases associated with the polymocleotide dysfunction, e.g. obesity or chronic obstructive pulmonary XX
XX
Claim 1; Fig 1; 145pp; English.

XX
Claim 1; Fig 1; 145pp; English.

XX
Craim 1; Fig 1; 145pp; English.

XX
Crass polymocleotide and polymocleotide and polymocleotide of the short kinase polymocleotide dysfunction. The expression vector or the cagent is useful in the preparation of a medicament for modulating the creating ty also be used for treating obsestivy overweight associated controlatines, such as obsestivy or chronic obstructive pulmonary disease.

CC may also be used for treating obsestivy overweight associated combidities, such as hypertension, diabetes, coronary artery disease, comorbidities, such as hypertension, diabetes, coronary artery disease, comorbidities, such as hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke, gallbladder disease, gout, osteoarthritis, sleep CC apnea, cancer, thrombolic diseases, polycystic ovarian syndrome, reduced XX
Sequence 1485 BP; 373 A; 353 C; 372 G; 387 T; 0 U; 0 Other;
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Sequence 1485 BP; 373 A; 353 C; 372 G; 387 T; 0 U; 0 Other;

Query Match

97.8%; Score 1481.8; DB 10; Length 1485;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1483; Conservative 0; Mismatches 2; Indels 0;

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Gaps

1026 1020 1086 1080 1146 1140 1206 1200 1266 1260 1326 1320 1386 1380 1446 1440 999 99 726 720 786 780 846 840 906 900 996 960 9 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGTGTTTT GGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC ccagarracargecrecreaagrecreacrergargaacgeggarggaaaagecaccrac GGCCTGGACTGTGACTGGTGGTCAGTGGGCGTGATTGCCTATGAGATGATTTATGGGAGA TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG TCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGGGG TTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC TITITIGAAATTTCCAGATGACCCCCAAAGTGAGCAGTGACTTTCTTGATCTGATCTGATCAAAGC TTGTTGTGCGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCTACCTTTCTTC 1021 TIGTIGIGGGCCAGABAAGAGAGTCTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC TCTAAAATTGACTGGAACAACATTGGTAACTCTCCCCCCCTTCGTTCCCACCCTCAAG 1081 rerahahridaeredaheaheariteerierereereeeeeeriteerieereeeaee 1141 TCTGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTTCG 1201 ccereccaecreaececercaeecrrereeegreaaeaacreecerrrereeegrrrree GTCGGGTCTGGACTCC CCTGCCAAGACTAGCTCCATGGAAAAAAAACTTCTCATCAAAAAGCAAAGAGCTACAAGAAC CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAAGAGAGGTACAAGAC TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTAC TCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 1485 ATCCTCCCGTCCGTATATGCCAAGGGATCCGCCCGGGGCCGCTGC TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCT 541 841 1027 1087 1147 1267 1261 1327 1321 1441 607 299 661 727 721 787 781 847 907 901 697 196 1447 1207 1387 유 셤 à 셤 셤 ઠ 셤 à 셤 à 셤 à 셤 셤 셤 рр 요 g à 셤 ò 셤 ਨੇ 8 ઢ ò ò à ò ð

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acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardovascular; hypertensis; drug screening; myocardial infarction; Goodpature's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hIV; neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic; hyperlipidaemia; enzyme; gene; ss.
Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;
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Homo sapiens

/\*tag= a /product= "Human kinase (PKIN)-21" Location/Qualifiers 55. .6219

WO200233099-A2

25-APR-2002

20-OCT-2001; 2001WO-US047728

2000US-0242410P 2000US-0244068P

2000US-0245708P. 2000US-0247672P. 2000US-0249565P. 2000US-0252730P. 20-OCT-2000; 27-OCT-2000; 03-NOV-2000; 09-NOV-2000; 16-NOV-2000;

22-NOV-2000; 01-DEC-2000;

(INCY-) INCYTE GENOMICS INC

ğ La] Arvizu C; n R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C; Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB; R, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, SA, Lu DAN, Borowsky ML, Thornton M, Swarnaker A; Recipon SA, Lu DAM, Borowsky ML, Thangavelu K, Khan FA, Ison CH; Gururajan R, Ŗ, Yao MG, Gandhi

WPI; 2002-454603/48.

P-PSDB; AAE24150.

New human kinase polypeptide, for diagnosing, preventing and treat cancer, immune system disorders, growth and development disorders cardiovascular disorders and lipid disorders.

5; Page 207-209; 210pp; English. Claim

The invention relates human kinases (PKIN) and their corresponding nucleic acid sequences. PKIN and its DNA are useful for diagnosing, treating and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (AIDS), Addison's disorder (e.g., acthma, atherosclerosis, multiple sclerosis, psoriasis), disorders affecting growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis), cardiovascular disorder (e.g., hypertension, myocardial infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver, Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver, Hypertlipidemaia, obesity), and a lipid disorder (e.g., fatty liver, Goodpasture's disease, Niemann-Pick's disease, hypercholesterolaemia, chosily, and a lipid disorder (e.g., fatty liver, Goodpasture's disease, wiemann-Pick's disease, hypercholesterolaemia, compounds Anti-PKIN antibody is useful in a disponseic test for a condition or a disease associated with the expression of PKIN in a should a suspending a disease or condition associated with decreased or increased expression of functional PKIN.

EXEMPLY IN SECTION OF AID STATE OF STATE PKIN CDNA

Sequence 6298 BP; 1772 A; 1585 C; 1720 G; 1221 T; 0 U; 0 Other;

1020 1008 ö 348 408 120 168 180 228 240 288 300 360 420 468 480 528 540 588 600 648 99 708 720 780 828 840 900 948 960 108 768 888 9 109 CCCATTGCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATG Grcagaagrcrrgraggrrgrggrcacrrrgcrgaagrgcaggrggraagagaaagca ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG 49 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGCTGTAA CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATG 169 ACTCAACAGCAGATGTCTCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 229 TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG **AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA** GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAGCA **ACCGGGGACATCTATGCTATGAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG** GTTTCATTTTTGAGGAAGAGGGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC GTTTCATTTTTTGAGGAGAAGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC GGAGGGGCTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 589 GGAGGGGACTTGCTCTCTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA CAGTTTTACCTAGCTGAGCTGATTTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG 649 CAGTTTTACCTAGCTGAGCTGATTTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTG GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT GATITIGGAICTGCCGCGAAAATGAATICAAACAAGAIGGIGAAIGCCAAACTCCCGATI GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGC GGGACCCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGTGTTGAACGGGGATGGAAAAGGC 841 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGCGTGATTGCCTATGAGATGATTAT 889 ACCTACGGCCTGGACTGTGACTGGTGGTCAGTGGCCGTGATTGCCTATGAGATGATTAT GGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC GGGAGATCCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTC CAGCGGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1009 CAGCGGTTTTTGAAATTTCCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT CAAAGCTTGTTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT 1069 CAAAGCTTGTTGTGCGGCCAGAAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCT Gaps ö Indels ë Mismatches ö Matches 1406; Conservative ч 121 241 301 349 361 961 61 289 409 529 1021 181 421 469 541 709 694 829 901 949 481 601 661 721 781 g 셤 셤 g 셤 a g g a g ઠે ઠે ò 8 ð ò ઠે 8 ò ò 셤 ò 원 g ઠે 엄 8 셤 ଚ 셤 8 셤 ઠ ð 8

> Length 6298; . 9 8 1404.2; No. 0; Score Pred. 92.7%; 99.8%; Query Match Best Local Similarity

2002US-0373826P 2002US-0373884P 2002US-0374977P 2002US-0381037P 2002US-0381038P 2002US-0381042P

22-APR-2002; 16-MAY-2002; 16-MAY-2002; 19-APR-2002;

19-APR-2002;

16-MAY-2002;

17-MAY-2002 28-MAY-2002

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TICTICICIAAAATIGACIGGAACAATICGIAACICTCCCCCCCTTCGTTCCCACC 1140
                CTCAAGTCTGACGATGACACCTCCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCA 1248
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                                                                                                        TITICGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTG 1320
                                                                                                                                                         GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCAAAAAAGCAAAGGCTA 1380
                                                                                                                                                                                                        GACTCCCCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGGCTA 1428
                                                                                           TCCTCTCCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGG
                                            CTCAAGTCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                           immunomodulator; cytostatic; notropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neeurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                  human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
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2001US-0328056P.
2001US-0328849P.
2001US-0329414P.
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2001US-0327917P.
2001US-0328029P.
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2001US-0327435P.
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09-0CT-2001; 2
12-0CT-2001; 2
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The present into asseribes Nova process, where A can be 1 to 35 described above and a carrier; (2) a kit comprsising in one or more described above and a carrier; (2) a kit comprsising in one or more containmers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX procein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically brinds to the polypeptide described above; (7) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above collypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or a berrant physiological interactions of the polypeptide; (11) a method of corrections of the polypeptide; (11) a method of corrections of the polypeptide; (11) a method of corrections or preventing a pathology associated with the above polypeptide; NovX asquences have antidiabetic, anorectic, antibacterial, virucide, and and antilipaemic activities, and can be used in gene therapy. The collypeptide is useful in manufacturing a method corrections, captometring a metabolic corrections, captometring a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dipippo VA;
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                                                                                                                                                                                                                                                                                                                                                                       Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Jiw, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes NOVX proteins, where X can be 1 to 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders such as Alzheimer's disease or Parkinson'
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DB 8; Length 1870;

Score 1398.2; Pred. No. 0; Pred. No. 0; 0; Mismatches

Query Match Best Local Similarity 99.8%; Matches 1400; Conservative

Sequence 1870 BP; 505 A; 416 C; 496 G; 453 T; 0 U; 0 Other;

2001US-0341058P

-OCT-2001; 17-OCT-2001; -OCT-2001; 2001US-0346357P

01-NOV-2001; 17-APR-2002;

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TCTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCTCAAG
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1266 1326 1213 1273 1333 1386 1153 1393 may for gene The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine Kinases, particularly Citron rho-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polynucleotides have a use in gene therapy. The encoded novel polypeptides are useful Human; kinase; enzyme; serine-threonine kinase; nootropic; cytostatic; Citron rho-interacting kinase; gene therapy; mental disorder; cancer; CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGGAAAGAGCTACAAGAC 1334 CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGAGCTACAAAAGA 1094 TCTAAAATTGACTGGAACAACATTCGTAACTCTCCCCCCCTTCGTTCCCACCCTCAAG TCCGACGATGACACCTCCAATTTTGATGAACCAGAGAAGAATTCGTGGGTTTCATCCTCT 1154 TCTGACGATGACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCATCCTCT CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG 1214 ccgreccaecreaeccercaecerreresegreaagaacreccerrreresegrirres TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGGTCTGGACTCC 1274 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTGGGGTCTGGACTCC Novel polynucleotide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, in therapy of disorders and diseases e.g. cancer and pharmacogenomic applications.

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generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The sequence encodes a novel human kinase of the invention
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                                                                                       Score 1398.2;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.8%;
Matches 1400; Conservative
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547 GACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATACAGTTT

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New human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or
                                                             invention relates to an isolated polynucleotide encoding a human
                                            Disclosure, Page 217-222; 237pp; English
                           Alzheimer's disease
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The invention relates to an isolated polyphocitice and number of circon rho/rac-interacting kinase polypeptide. The isolated polymucleotide comprises a 6165 or 8603 base pair sequence, given in the polymucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human circon rho/rac-interacting kinase (CRIKI)

polypeptide and polymucleotide are useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction such as obesity associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breat, prostate and colon cancer).

CC cancer including endometrial, breat, prostate and colon cancer, of isoacers, anxiety disorders, Parkinson's disease or Alzheimer's cancer including contractive pulmonary disease, or diabetes. These can disoase, critoric obstructive pulmonary disease, or diabetes. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing.

The expression vector or the reagent is useful in preparing a medicament of modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a CRIK polypeptide and for use in various assay systems. The methods are useful in producing and detecting the polymucleotide and polypeptide and in solymucleotide sequence represents a DNA sequence relating to the human CRIK protein of the invention

Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;

ö 486 TTTTTGAGGAAGAGGGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA 480 546 CAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG 540 126 186 246 240 306 366 426 GCCAGCCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGAAACCACCCTTTATGACTCAA 120 CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA 180 TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA 300 AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAGCAACCGGG 360 GACATCTATGCTATGAAAGTGATGAAGAAGAGGCTTTATTGGCCCAGGAGCAGGTTTCA 420 99 9 ATGTTGAAGTTCAAATATGGAGGGGGGAATCCTTTGGATGCTGGTGCTGCTGAACCCATT ATGTTGAAGTTCAAATATGGGGGGGGGGGAATCCTTTGGATGCTGGTGCTGCTGCTGAACCCCATT GCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATGACTCAA CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA GAATGCAGTCAGCCTGCTCTGATGAGGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT TCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAAGTCAGA AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGGAGAAAGCAACCGGG TTTTTGAGGAAGAGGGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCCCAATTA CAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCTGGAGGG GAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGGAAGTAT GACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGCCCCAGGAGCAGGTTTCA Gaps Length 6156; ö 3; Indels Score 1398.2; DB 9; Pred. No. 0; 0; Mismatches 3; 1 92.3%; Best Local Similarity 99.8 Matches 1400; Conservative 241 7 61 121 181 487 481 Query Match 67 127 187 247 307 301 367 361 427 421 g 셤 ઠે g 셤 유 g 셤 δ 셤 ሯ ઠ ઠે ઠે ઠે ઠ ઠે

<u>8</u>	541 G	GACTIGCTOTCACTITICACTICACACTOR AND
à	607 T	TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTGCATCGA 666
qa	601 T	ACCTAGCTGAGCTGATTTTGGCTGTTCACAGGTTCATCTGATGGGATACGTGCTCGA 660
& A	667 G 661 G	GACATCAAGCCTGAGAACATTCTCGTTGACCGCACAGGACACATCAAGCTGGTGGATTTT 726 
ò	727 G	GGATCTGCCGCGAAAATGAATTCAAACAAGGTGAATGCCAAACTCCCGATTGGGACC 786
q	721 G	GATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATTGGGACC 780
දු පු	787 C	CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGCACCTAC 846
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q	841 G	GCCTGGACTGTGACTGGTGGTCAGTGGCGTGATTGCCTATGAGATGATTATAGGGAGA 900
ò	907 T	TCCCCTTCGCAGAGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCG 966
g	901 T	CCCCCTTCGCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTTCCAGCGG 960
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đ	961 T	TTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATTCAAAGC 1020
ờ	1027 T	TTGTTGCGCCCAGAAGAGACTGAAGTTTGAAGCTCTTTGCTGCCATCCTTTCTTC 1086
đ	1021 T	TGTTGTGCGCCCAGAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC 1080
ò	1087 T	TCTAAAATTGACTGGAACATTCGTAACTCTCCCCCCCTTCGTTCCCACCCTCAAG 1146
đ	1081	CTAAAATTGACTGGAACAACATTCGTAACTCTCCTCCCCTTCGTTCCCACCCTCAAG 1140
ò	1147 T	
q	1141 T	crdacgardacdecreccarrrrgardadecagagaadaarregregerrreareerer 1200
δ	1207 C	CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCCGTTTGTGGGGTTTTTCG 1266
q	1201 C	CGTGCCAGCTGAGCCCCTCAGGCTTTTCGGGAGAACTGCCGTTTGTGGGGGTTTTCG 1260
ò	1267 T	TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGTTGTTGTGTCGGGTCTGGACTCC 1326
d d	1261 T	ACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTGGGGTCTGGACTCC 1320
ò	1327 C	CCTGCCAAGACTAGCTCCATGGAAAAGATTCTCATCAAAAGCAAAGAGCTACAAGAC 1386
QQ	1321 ¢	creccaagacragerecarggaaaagaaacrrerearcaaaagcaaagagraaagae 1380
ò	1387 T	TCTCAGGACAAGTGTCACAAGGT 1409
q	1381 T	CTCAGGACAAGTGTCACAAGAT 1403
REST ABQ7 ID	RESULT 11 ABQ78870 ID ABQ78870 s	tandard; cDNA; 6165 BP.
ž ž	ABQ78870;	
\$ E \$	10-OCT-200	2 (first entry)
名 第 日 第	Human kinas	se cDNA #1.
Z Z	Human; kin Citron rho	kinase, enzyme, serine-threonine kinase, nootropic, cytostatic, rho-interacting kinase, gene therapy, mental disorder, cancer;

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CCGTGCCAGCTGAGCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCG
                               AGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAAAAGCAACCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel human protein that shares structural similarity with animal kinases, including serine-threonine kinases, particularly Citron the-interacting kinases. The proteins of the invention have nootropic and cytostatic activity. The polymucleotides may have a use in gene therapy. The encoded novel polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NMP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases including cancer. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide encoding human proteins that are structurally similar to animal kinases, useful for drug screening, diagnosis, ir therapy of disorders and diseases e.g. cancer and pharmacogenomic
                                                                                                                                                                                                /standard_name= "Single nucleotide polymorphism"
                                                                                                                                                  nucleotide polymorphism'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6165 BP; 1735 A; 1550 C; 1679 G; 1201 T; 0 U; 0 Other;
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Pred. No. 0;
0; Mismatches
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                                                                          1. .6165
/*tag= a
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replace(5218,G)
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                                                          Location/Qualifiers
1. .6165
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Best Local Similarity 99.8%;
Matches 1400; Conservative 0
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P-PSDB; ABB81927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynuclectide encoding a human citron rho/rac-interacting kinase polypeptide. The isolated polynucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide are useful in preventing, ameliorating, creating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, postere and colon cancer), anorexia, cachexia, bullimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, Parkinson's disease or Alzheimer's disease, chronic obstructive pullmonary disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in disgnostic assays or in genetic testing. The expression vector or the reagent is useful in preparing a medicament for modulating the activity of a human CRIK in a disease, e.g. obesity, a central nervous system disorder, or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human citron rho/rac-interacting kinase (CRIK) polypeptide and polynucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or
                                                                                                                                                                                                                                 Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective; antiaqut; osteopathic; antiarthritic; cytostatic; antidepressant; immunomodulator; antianalic; tranquiliser; antiparkinsonian; nootropic; neuroprotective; antiinflammatory; antidiabetic; analgesic; human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating; obesity; comorbidities, cancer; anorexia; cachexia; bulimia; central nervous system disorder; chronic obstructive pulmonary disease; diabetes; pain; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .6165
/*tag= a /product= "Human CRIK protein"
                                                                                                                                                                                                       Human CRIK encoding DNA sequence, SEQ ID No 1.
                               1403
 1409
TCTCAGGACAAGTGTCACAAGGT
                  TCTCAGGACAAGTGTCACAAGAT
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11-DEC-2001; 2001US-0338651P.
25-APR-2002; 2002US-0375014P.
                                                                                                           AAL55214 standard; DNA; 6165
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                                      useful in producing and detecting the polynucleotide and polypeptide and in screening for agente that modilate the activity of the human CRIK polypeptide. This polynucleotide sequence represents a DNA sequence encoding a human CRIK protein of the invention
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781 CCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAGGCACCTAC
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                                                                                                                                                                                                    92.3%; Score 1398.2; DB 9; Length 6165; 99.8%; Pred. No. 0;
                                                                                                                                                           Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;
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CRIK polypeptide and for use in various assay useful in producing and Astroction
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Anorectic; hypotensive; cardiant; antilipaemic; cerebroprotective; antigout; osteopathic; antiarthritic; cytostatic; antidepressant; immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic; neuroprotective; antihnflammatory; antidiabetic; analgesic; human citron rho/rac-interacting kinase; enzyme; CRIK; ameliorating; obesity; comorbidites, cancer; anorexia; cachexia; bulimia; central nervous system disorder; chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                                                               Human CRIK related DNA sequence, SEQ ID No 4.
                                                                          BP
                                                                          AAL55215 standard; DNA; 8603
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RESULT
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2001US-0338651P.
2002US-0375014P.
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                                                                                                  02-JUL-2001; 2
11-DEC-2001; 2
25-APR-2002; 2
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                                                                     Homo sapiens
                                                                                    16-JAN-2003.
                                                                                                                  (FARB )
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WPI; 2003-221576/21

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The invention relaters to an institute parymentolite incolling a numbar citron rho/rac-interacting kinase polypeptide. The isolated polymucleotide comprises a 6165 or 8603 base pair sequence, given in the polymucleotide comprises a 6165 or 8603 base pair sequence, given in the specification. The human citron rho/rac-interacting kinase (CRIK) or polypeptide and polymucleotide are useful in preventing, ameliorating, or treating diseases associated with human CRIK dysfunction such as obesity and obesity-associated comorbidities (e.g. hypertension, coronary artery disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of cancer including endometrial, breast, prostate and colon cancer).

CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood disorders, anxiety disorders, parkinson's disease, or diabetes. These can also be used to treat pain associated with the disorders. The human CRIK polypeptide is also useful in diagnostic assays or in genetic testing.

CT he expression vector or the reagent is useful in preparing a medicament control systems. The fusion protein is useful for generating antibodies against a central nervous system disorder; or chronic obstructive pulmonary disease. The fusion protein is useful for generating antibodies against a cuseful in producing and detecting the polymucleotide and dot use in various assay systems. The methods are cuseful in producing to the human CRIK protypeptide and corecting the polymucleotide and polymucleotide sequence represents a DNA sequence corelitating to the human CRIK protein of the invention
New human citron rho/rac-interacting kinase (CRIK) polypeptide and polymucleotide, useful in preventing, ameliorating or treating diseases associated with human CRIK dysfunction, e.g. obesity, diabetes or
                                                                                                                                                                                                                                 invention relates to an isolated polynucleotide encoding a human
                                                                                                                                                                  Disclosure; Fig 4; 237pp; English
                                                                                                             Alzheimer's disease.
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Gaps DB 9; Length 8603; ; 0 Sequence 8603 BP; 2305 A; 2206 C; 2215 G; 1877 T; 0 U; 0 Other; 3; Indels Query Match 92.3%; Score 1398.2; Best Local Similarity 99.8%; Pred. No. 0; Matches 1400; Conservative 0; Mismatches

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/\*tag= a
19. .6180
/\*tag= b
/product= "Human MDPK protein"
19. .6177
/\*tag= c
/\*tag= c
solution is specifically referred in claim 1
as SEQ ID NO:3"
6181. .6574
/\*tag= d
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Location/Qualifiers

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skeletal muscle disorder; muscular dystrophy; myotonic dystrophy;
immune disorder; neoplastic disorder; gene therapy; gene; ss.
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                                                                                                                                                                                                                                                                               23-OCT-2000; 2000US-0242429P
                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
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P-PSDB; AAE24079.
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                                                                                                                                                                                                                                 The invention relates to human myotonic dystrophy type protein kinase (MDPK) polypeptides designated as 13245 and nucleic acid molecules encoding such polypeptides. 13245 molecules are used to develop diagnostic and therapeutic agents for prognosticating, diagnosing, preventing, inhibiting, alleviating or curing MDPK-related disorders. Polypeptides of the invention are used to develop diagnostic and therapeutic agents for 1345-mediated or related disorders uch as tumour growth, tumour metastasis, viral infection of a cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies), immune disorders and neoplastic disorders. The invention is also used in
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Human myotonic dystrophy type protein kinase polypeptide and polynucleotide useful for prognosticating, diagnosing, preventing inhibiting tumorigenesis, tumor growth, tumor metastasis and viral
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92.3%; Score 1397.8; DB 6; Length 6574;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 7; Indels 0:
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                                                                                                                                                                     Claim 1; Fig 1; 148pp; English.
                                                                                                        infection.
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AAD39191 standard; cDNA; 6574 BP

AAD39191 RESULT

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AAD39191;

Human MDPK cDNA.

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Human, myotonic dystrophy type protein kinase; MDPK, 13245 protein; tumourigenesis; tumour growth; tumour metastasis; viral infection;

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The present invention relates to a method for identifying a compound capable of modulating pain or painful disorders. The method comprises sasaying the ability of the compound to modulate specific nucleic acid expression or polypeptide activity eg. potassium channel, or kinase expression/activity. The method and compounds are useful for treating pain or painful disorders e.g. inflammatory pain, chronic pain, neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache pain and tissue pain. The present sequence encodes a human protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a compound capable of treating a pain disorder comprises assaying the ability of the compound to modulate specific, e.g., kinases or potassium channel, nucleic acid expression or polypeptide activities.
                                                                                                                                                                                                                                                                                                                                                                                     Pain modulation; pain disorder; painful disorder; potassium channel; kinase expression; inflammatory pain; chronic pain; neuropathic pain; causalgia; fibromyalgia; cancer pain; migraine; headache; tissue pain; analgesic; antlinflammatory; gene; ds.
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1 (bases 1 to 1515)
Webster, M., Yan, C., Di Francesco, V. and Beasley, E.M.
Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof Patent: US 6479269-A 1 12-NOV-2002;
Location/Qualifiers
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Gandhi, A.R., Tribouley, C.M., Walia, N., Yao, M.G., Lu, D.A.,
Grenwald, S.R., Ramkumar, J., Griffin, J.A., Kearney, L., Burford, N.,
Nguyen, D.B., Tang, Y.T., Baughh, M.R., He, A., Thornton, M.,
Hafalia, A., Patterson, C., Gururajan, R., Lo, T.P., Khan, F.,
Recipon, S.A., Azimzai, Y., Policky, J.L., Ding, L., Grether, M.,
Humain kinaes
Bliott, V.S., Thangavelu, K., Batra, S. and Ison, C.H.
Humain kinaes
Patent: WO 01096547A 33 20-DEC-2001;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/mol_type="unassigned DNA"
/mol_trye="taxon:9606"
/note="Incyte ID No: 3951059CB1"
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99.8%; Pred. No. 0;
cive 0; Mismatches
              AX642956 2066 bp 1
Sequence 33 from Patent WO01096547.
AX642956
                                                        AX642956.1 GI:28550096
                                                                                   sapiens (human)
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Best Local Similarity 99.8°
Matches 1512; Conservative
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RESULT 4
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Regulation of human citron rho/rac-interacting kinase-short Patent: WO 03004629-A 1 16-JAN-2003;
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/db_xref="taxon:9606"
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   Length
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Score 1481.8;
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121 ACTCAACAGCAGATGTCTCCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 180  169 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 228  181 TTTGAAGAATGCTCCTCTTTCCCGAGAAGGATTAAGCAGCTCTTTGTTCTC 228  181 TTTGAAGAATGCAGTCCTGCTCTGATGAGATTAAGCAGTGAGCAATTTGTCCGG 240  229 TTTGAAGAATGCAGTCAGCCTCTCTTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG 288  241 AAGTATTCCGAACACAACAGAGTTACAGGAGCTCCAGCCTTCGACAAAGGACTTCGAA 348  289 AAGTATTCCCAACACCATAGCTGATTACAGGAGCTCCCAGCCTTCGACAAAGGACTTCGAA 348		. 4. 10 10 10	1 GGAGGGGACTTGCTCTCTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 60		GATTTTGGATCTGCCGCAAATGAATTCAACAAGTGGTGAATGCCAACTCCCGATT 8 GGGACCCCAGATTACATGCTCCCTGAAGTGCTGATGAACGGCGAAAGGC 8 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGATGAACGGGGGGCGGGC	841 ACCTACGGCCTGGACTGGTGGTGGGTGATGGCTGATGGGTGATTGT 900	961 CAGCGGTTTTTGAAATTTCCAGATGACCCCAAAGTGAGCAGTGACTTTCTTGATCTGATT 1020	CAAAGCTTGTTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCATCCT TTCTTCTTGCTGCGCATCCT TTCTTCTCTAAAATTGCTGCGAACAACATTGAAGCTTCGTAAGTTGAAGGTTCCTTGTAAGTTGCTGCACC TTCTTCTCTTAAAATTGACTGGAACAACATTCGTAAGCTTCCTCCTCCCCCCTTCGTTCCTAGTTCTTCTTCTTCTTCTTCTTCGTTCCTTCGTTCG	1141 CTCAAGTCCGACGATGACACCTCCAATTTGATGAACCAGAGAAGAATTCGTGGGTTTCA 1200
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Oy 1027 TTGTTGTGGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC 1086  1021 TTGTTGTGCGGCCAGAAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC 1080  Qy 1087 TCTAAAATTGACTGGAACAACTTCGTAACTCTCCCCCCTTCGTTCCCACCTTAAG 1146  Db 1081 TCTAAAATTGACTGGAACAACTTCGTAACTCTCCCCCCTTGGTTCCTAAG 1140  Qy 1147 TCCGAACATGACACACTTCTAAAATTGATGAACAAGAAATTCGTGGGTTTCATCCTCT 1206  Db 1141 TCTGAACATGACACCTCCCAATTTTGATGAACAAGAGAATTCGTGGGTTTCATCCTCT 1200  Db 1141 TCTGAACACCTCCCAATTTTGATGAACAAGAGAATTCGTGGGTTTCATCCTCT 1200	1207   CCGTGGCCAGGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTTCG	1261 1327 1321 1381		RESULT 6 AX604254 AX604254 LOCUS DEFINITION Sequence 43 from Patent W00233099. ACCESSION AX504254 VERSION AX504254. GI:23386094 KEYWORDS SOURCE Homo sapiens (human)	NISM Homo sapiens Eukaryota; Me Mammalia; But NCE 1 ORS Gururajan, R., Arvizu, C., Ya	Tribouley, C.M., Lal, P.G., Recipon, S.A., Lu, D.A., Borowsky, M.L., Thornton, M., Swarnaker, A., Thangavelu, K., Khan, F.A. and Ison, C.H. TITLE Human kinases JOURNAL Patent: WO 0233099-A 43 25-APR-2002; Incyte Genomics, Inc. (US) FEATURES Location/Qualifiers Source 1. 6298	/organim="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="Incyte ID No: 7484498CB1"	Query Match  Best Local Similarity 99.8%; Pred. No. 0;  Best Local Similarity 99.8%; Pred. No. 0;  Matches 1406; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 1 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGAA 60	TTATG

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ALNDELLEKERQWEAMRSVLGDEKSQFECRVRELQRWLDTEKQSRARADQRI TESRQV
VELAVERHVAET LALQQALKEQKLKAESLSDKLTMDLEKKHAMLENNARSLQQKLETER
ELKQRLLEGAKLLQQQNDLQWHH TRLTQGLGLBADLLAKTERSDLEYQLBLQRAL
YSHEKVIRMEGTI SQQTKLI DFLQAKMDQPAKKKKGLFSRRKEDPALPTQVPLQVPLEK
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RLREVSLEHEEQKLELKROLTELQLSLQERESQLTALQAARAALBSQLRQAKTELEET
TAEAEEEIQALTAHRDEIQRKPDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSK
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1 (bases 1 to 8576)

Huang, C.Q., Wu, S.L., Shan, Y.X., Liu, S. and Xiao, P.J.

Direct Submission

Direct Submission

Submitted (18-MAR-2003) Department of Biochemistry and Molecular Biology, Basic Medicine, Suzhou University, Renming Road 48, Suzhou, Jiangsu 215007, China

Location/Qualifiers

1. 8576

//crganism="Homo" sapiens"
                                                                                                                                   TTTTCGTACAGCAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCTCGGGTCTG
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/db_xref="taxon:9606"
/chromosome="12"
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/note="synonym: CRIK"
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CLDTVHFGRAGSKCLECQWMCHPKGSTCLPATCGLPAETATHFTBAFCRDKWNSPGLO
TKEPSSSLHLEGWWKU-PRINKRGGOWDRKT YULGGSKVLI YDNEAREAGORPWEFBF
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HFNSLEVLIGTREGRAYPOTSCORPANTICPHEGRANTALSSYQDKLRVICCKG NLVKESGTEHHRGPSTSRSSPNKRGPPTYNEHITKRVASSPAPPEGPSHPREPSTPHR YREGRTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVRTPLS ô 120 360 107 180 240 288 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 347 420 467 480 540 287 241 AAGTATTCCGACACCATAGCTGAGTTACAGGAGCTCCAGCCTTCGGCAAAGGACTTCGAA 300 407 527 587 9 647 999 108 CCCATTGCCAGCCGGGCCTCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 167 168 ACTCAACAGCAGATGTCTCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC 227 707 9 48 GGGGAGATGTTGAAGTTCAAATATGGAGCGCGGAATCCTTTGGATGCTGGTGCTGCTGAA CCCATTGCCAACCGGGCCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACCCTTTATG 228 TITGAAGAATGCAGTCAGCTCTGATGAAGATTAAGCACGTGAGCAACTITGTGGG 348 GTCAGAAGTCTTGTAGGTTGTGGCTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAAGCA GTCAGAAGTCTTGTAGGTTGTGGTCACTTTGCTGAAGTGCAGGTGGTAAGAGAGAAGCA ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG ACCGGGGACATCTATGCTATGAAAGTGATGAAGAAGAAGGCTTTATTGGCCCAGGAGCAG 648 cacrirraccradereacrearrirecererreacaccerrearerearecaracere 121 ACTCAACAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTC TTTGAAGAATGCAGTCAGCCTGCTCTGATGAAGATTAAGCACGTGAGCAACTTTGTCCGG GTTTCATTTTTGAGGAAGAGCGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC 468 GTTTCATTTTTGAGGAAGAGGGGAACATATTATCTCGAAGCACAAGCCCGTGGATCCCC CAATTACAGTATGCCTTTCAGGACAAAATCACCTTTATCTGGTCATGGAATATCAGCCT 528 CAATTACAGTATGCCTTTCAGGACAAAAATCACCTTTATCTGGTCATGGAATATCAGCCT GGAGGGGACTTGCTGTCACTTTTGAATAGATATGAGGACCAGTTAGATGAAAACCTGATA 601 CAGTTTTACCTAGCTGAGCTGATTTTGGCTGTTCACAGCGTTCATCTGATGGGATACGTG Gaps ö Length 8576; Indels DB 9; 3, Score 1404.2; Pred. No. 0; 0; Mismatches QVNKVWDQSSV" 92.7**%**; 99.8**%**; Conservative Similarity Best Local Simi Matches 1406; 181 361 408

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781 GGGACCCCAGATTACATGGCTCCTGAAGTGCTGACTGTGATGAACGGGGATGGAAAAGGC 840

768 GATTTTGGATCTGCCGCGAAAATGAATTCAAACAAGATGGTGAATGCCAAACTCCCGATT

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108 CATCGAGACATCAAGCCTGAGAACATTCTCGTTGACCGCACACAGGACATCAAGCTGGTG 767

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QCGHPAELQVQVRRKATGDIJYAMKVWKKKALLAQEQVSFFEEERNILSRSTSPWIPQL
QYAFQDROHLYLVMSVOPGGDILSLINRYEDQLDENLIOFYLAELILAVHSVHLMGYI
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KNSWYSSSPQQLSPGGFSGEELPFVGFSYSKLGILGRSESVVSGLDSPAKTSSMEKK
LLIKSKELQDSQDKCHKMEQEMTRLHRRVSGG"
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/protein_id="AAP43922.1"
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Bukaryotreus

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mao, Y., Xie, Y. and Wu, Q.

Cloning and characterizing a novel human CRIK-SK gene
Unpublished

2 (Bases 1 to 1799)

Mao, Y., Xie, Y. and Wu, Q.

Direct Submission

Submitted (02-JAN-2003) Institute of Genetics, Fudan University,
220 Handan Road, Shanghai 200433, P.R. China

Location/Qualifiers
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/mol_type="mRNA"
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/note="protein kinase"
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	Oy         727 GGATCTGCCGCGAAATGAATTCAAACAAGATGTGAATGCCAAACTCCCGATTGGGACC         786           Db         721 GGATCTGCCGCGAAAATGAATTCAAACAAGATGCTGAATGCCCAAACTCCCGATTGGGACC         780           Oy         787 CCAGATTACATGGCTCCTGAAGTGCTGATGAAAGGCACCTAC         846           Db         781 CCAGATTACATGGCTCCTGAAGTGCTGATGAAAGGCACCTAC         840           Oy         847 GGCCTGGACTGGTCAGTGACTGTGATGAAAGGGAAAGGCACCTAC         840           Db         841 GGCCTGGACTGTGATGAGTGAGAGGGATTGATATATTATGGAGA         906           Oy         907 TCCCCCTTGACTGACTGGTGAACCTTCAATAACATTATGATTATGGAGA         900           Oy         907 TCCCCCTTGGCAGAGGGAACCTTGCCAGAACCTTCAATAACATTATGAATTCCAGCGG         966           Oy         967 TTTTTGAAATTTCCAGAGGGAACCTCTGCCAGAACCTTCAATAACATTATGAATTCCAGCGG         960           Oy         967 TTTTTGAAATTTCCAGAGGGAACCTCTGCCAGAGCTTCAATAACATTATGAATTCCAGCGG         960           Db         961 TCCCCCTTCGCAGAGGGAACCCCCAAAGTGAGCAGTGAGAGTATTCTTGATTCAATACATTATCAATACATTCAAAACTCAATACAATTCAAAACTCAATACAATTCAAAACTCAATACAATTCAAAACTCAATACAATTCAAAAGCTCAAAACTCAATACAATTCAAAACTCAATTCAAAACTCAAAACTCAATACAATTCAAAAACTCAATACAATTCAAAAACTCAAAAAA	QY         1027 TTGTTGTGGGGCCAGAAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC         1086           Db         1021 TTGTTGTGGGCCAGAAGAGAGACTGAAGTTTGAAGGTCTTTGCTGCCATCCTTTCTTC         1080           QY         1087 TCTAAAATTGACGAACAACTTCGTAACTCTCCCCCCCTTGGTCCCACCTTCATTCTTC         1080           Db         1081 TCTAAAATTGACGAACAACTTCGTAACTCCTCCCCCCCTTCGTTCCCACCTCAAG         1140           CD         1147 TCCGACGATGACACACTTTGAACACTTCCTCCCCCCCTTCGTTCCTCCTCCTCTCT         1206           Db         1141 TCTGACGATGACACTTCTGAACACACACACAGAAGAATTCGTGGGTTTCATCCTCT         1200           QY         1207 CCGTGCCAGTGAGCCCTCAGGCTTCTCGGGTGAAGAATTCGTGGGTTTTTTCG         1260           QY         1207 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTTCG         1260           QY         1261 TACAGCAAGAGCACTGAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG         1260           QY         1327 CCTGCCAAGTTCTTGGTAGATCTTGAGTCTGTTGTGTGGGGTTTTCG         1326           Db         1321 CCTGCCAAGACACTGGAAAAGAAAAGAAAGAAAGACAAAAGAAAG	AX671112 LOCUS AX671112 6156 bp DNA linear PAT 27-MAR-2003 DEFINITION Sequence 8 from Patent WO03004523.
QY         1207 CCGTGCCAGCTGAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGTTTTCG         1266           Db         1201 CCGTGCCAGCTGAGGCTTCTCGGGTGAAGAACTGCGTTTGTGGGGTTTTCG         1260           Db         1267 TACAGCAGCTGAGGATTCTTGGTAGATCTGAGTCTGTTGTCGGGTTTTCG         1360           Db         1261 TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGATCTG	AX574427  AX574427  AX574427  DEFINITION  Sequence 3 from Patent W002059325.  ACCESSION  AX574427.  GI:27551752  Home sapiens (human)  ORGANISM Home sapiens (human)  ORGANISM Home sapiens (human)  ORGANISM Home sapiens (human)  AMMERIANCE Home sapiens (Authority Hominidae; Home.  Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Home.  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home.  Mammalia; Eutheria; Drimates; Catarrhini; Hominidae; Home.  AMTHORS YU, X., Miranda, M. and Friddle, C.J.  TILLE Human kinases and polymucleotides encoding the same  JOURNAL Patent: W0 02059325-A 3 01-AUG-2002;  Lexicon Genetics Incorporated (US)  FEATURES  1. 5877  Corganism="Home sapiens"  //mol type="unassigned DNA"  //db_Xref="taxon:9606"	Duery Match  92.3%; Score 1398.2; DB 6; Length 5877; Best Local Similarity 99.8%; Pred. No. 0;  ArgirgaagricaaarargaaGcGGGAATCCTTTGGATGCTGGTGCTGAAC	

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E 1 (bases 1 to 6165)
AS Yu,X.S., Miranda M. and Friddle,C.J.
Human kinases and polymucleotides encoding the
Human kinases and polymucleotides encoding the
Tocation/Qualifiers
Location/Qualifiers
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                                                           Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Regulation of human citron rho/rac-interacting kinase Patent: WO 03004523-A 8 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Pred. No. 0;
0; Mismatches
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
                 GI:29329572
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                                             Homo sapiens (human)
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Best Local Similarity 99.8
Matches 1400; Conservative
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Catarrhini; Hominidae;
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Yu,X., Miranda,M. and Friddle,C.J.
Human kinases and polymucleotides encoding the same
Patent: WO 02059325-A 1 01-AUG-2002;
Lexicon Genetics Incorporated (US)
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Catarrhini; Hominidae; Homo.
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Regulation of human citron rho/rac-interacting kinase
Patent: WO 03004523-A 1 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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Pred. No. 0;
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    .6165
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                             AX671105 6165 bp
Sequence 1 from Patent WO03004523
                                                                                                                 Homo sapiens
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
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Best Local Similarity 99.8%;
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                 GACATCTATGCTATGAAAAGAAGAAGAAGGCTTTATTGGCCCAGGAGCAGGTTCA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Regulation of human citron rho/rac-interacting kinase Patent: WO 03004523-A 4 16-JAN-2003;
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Score 1398.2;
Pred. No. 0;
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  92.3%;
 Query Match 92.3
Best Local Similarity 99.8
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	/ TCTCAGGACAAGTGTCACAAGGT 1409	1387	ò
1380	CCTGCCAAGACTAGCTCCATGGAAAAGAAACTTCTCATCAAAAGCAAAGGGCTACAAGAC	1321	qa
1386	CCTGCCAAGACTAGCTCCATGGÄAAAGAAACTTCTCATCAAAAGCAAAGGCTACAAGGC	1327	ò
50	. TACAGCAAGGCACTGGGGATTCTTGGTAGATCTGATGTGTTGTGTCGGGTCTGGACTCC 1320	1261	g
1326	TACAGCAAAGGCACTGGGGATTCTTGGTAGATCTGAGTCTGTTGTGTCGGGTCTGGACTCC	1267	ò
09	. CCGTGCCAGCTGAGCCCCCTCAGGCTTCTCGGGTGAAGAACTGCCGTTTGTGGGGGTTTTCG 1260	1201	οg
1266	CCGTGCCAGCTCACAGCCTTCTCGGGTGAAGAACAACTGCCGTTTGTGGGGGTTTTCG	1207	ò
00		1141	đ
1206	TCCGACGATGACACCTCCAATTTTGATGAACCAGAGAATTCGTGGGTTTCATCTCT	1147	È
1140	TCTAAAATTGACTGGAACAATTCGTAACTCTCCTCCCCCCTTCGTTCCCACCCCCAGG	1081	đ
1146	TCTAAAATTGACTGGAACAATTCGTAACTCTCCCCCCCTTCGTTCCCAAG	1087	ò
1080	TIGHTHE	1021	qa
1086	TIGITGIGGGCCAGAAAGAGACIGAAGITIGAAGGICITIGCTGCCATCCITICITC	1027	ò

Search completed: March 19, 2005, 11:54:27 Job time : 6461.94 secs